



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 206221

TO: Quang Nguyen
Location: rem/2E81/2C70
Art Unit: 1633
Thursday, November 02, 2006
Case Serial Number: 10/706798

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161
Kristine.Hensle@uspto.gov

Search Notes

Examiner Nguyen,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

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OM nucleic - nucleic search, using sw model
 Run on: November 1, 2006, 19:39:18 ; Search time 1837.86 Seconds
 (without alignments)
 2887.948 Million cell updates/sec

Title: US-10-706-798-1
Perfect score: 83
Sequence: tcnuuggagaaaguagcgc. gcuugcucaaaaacaagg 83
Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

Genbank:
 1: gb_env:/*
 2: gb_pat:/*
 3: gb_ph:/*
 4: gb_pl:/*
 5: gb_pr:/*
 6: gb_ro:/*
 7: gb_sts:/*
 8: gb_sy:/*
 9: gb_un:/*
 10: gb_vl:/*
 11: gb_ov:/*
 12: gb_hhg:/*
 13: gb_in:/*
 14: gb_om:/*
 15: gb_ba:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	83	100.0	83	CS185098 CS185098 Sequence
2	83	100.0	83	CS188802 CS188802 Sequence
3	83	100.0	663	AY866304 AY866304 Lemur cat
4	83	100.0	712	AY866308 AY866308 Iagothrix
5	83	100.0	747	AY866306 AY866306 Pongo pyg
6	83	100.0	825	AY866302 AY866302 Saguinus
7	83	100.0	836	AY866299 AY866299 Atelopus ge
8	83	100.0	871	AY866301 AY866301 Macaca ne
9	83	100.0	896	AY866305 AY866305 Macaca mu
10	83	100.0	901	AY866300 AY866300 Gorilla g
11	83	100.0	902	AY866307 AY866307 Pan trogl
12	83	100.0	914	AY866303 AY866303 Pan panis
13	83	100.0	153092	AC059475 AC059475 Homo sapi
14	83	100.0	154868	AF334404 AF334404 Homo sapi
15	83	100.0	154887	ALU37060 ALU37060 Human DNA
16	83	100.0	184155	AC155017 AC155017 Bos tauru
17	83	100.0	235659	AC152429 AC152429 Bos tauru
18	83	100.0	347503	AF219660 AF219660 Homo sapi

DEFINITION Sequence 33 from Patent WO2005078139.		ORIGIN /product="microRNA mir-16-1"
ACCESSION CS188802.1		VERSION CS188802
KEYWORDS		Best Local Similarity 73.5%; Pred. No. 1.6e-20; Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0; Oligo 1
SOURCE		Homo sapiens (human)
ORGANISM		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buarchoptoglires; Primates; Catarhini; Hominidae; Homo.
REFERENCE		Croce, C.M.
AUTHORS		Patent: WO 2005078139-A 33 25-AUG-2005;
JOURNAL		THOMAS JEFFERSON UNIVERSITY (US)
FEATURES		Location/Qualifiers 1. .83
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Query		1 CCUUGGAGUAAGUAGCAGCCAUAAUGGUUGUGGAUUAAGGUAGGCCAUU 60
Db		1 CCTTGAGTAAGTAGCAGCACATATGGTTGIGGATTGAAAGGTCAGCCATAT 509
QY		61 UGGUGUGCCUAAAUACAGG 83
Db		61 TGTGCTGCCCTAAATACAGG 532
RESULT 3		RESULT 4
LOCUS AY866304		AY866308
DEFINITION Lemur catta microRNA mir-15a and microRNA mir-16-1 genes, complete sequence.		LOCUS AY866308
ACCESSION AY866304		DEFINITION Lagotrix lagotricha microRNA mir-15a and microRNA mir-16-1 genes, complete sequence.
VERSION AY866304.1		ACCESSION AY866308
KEYWORDS		VERSION AY866308.1
REFERENCE		KEYWORDS
ORGANISM		ORGANISM Lagotrix lagotricha (common woolly monkey)
TITLE		Lagotrix lagotricha
JOURNAL		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buarchoptoglires; Primates; Platyrhini; Cebidae; Atelinae; Lagotrix.
PUBLMED		REFERENCE 1 (bases 1 to 712)
AUTHORS		AUTHORS Bezeikov, E., Guryev, V., van de Belt, J., Wienholds, E., Plasterk, R.H. and Cuppen, E.
REFERENCE		REFERENCE 2 (bases 1 to 712)
TITLE		AUTHORS Bezeikov, E., Guryev, V., van de Belt, J., Wienholds, E., Plasterk, R.H. and Cuppen, E.
JOURNAL		TITLE Direct Submission
FEATURES		JOURNAL Submitted (28-DEC-2004) Hubrecht Laboratory, Uppsalaalaan 8, Utrecht 3584 CT, The Netherlands
Source		FEATURES Location/Qualifiers
ORIGIN		1. .712
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Db		/mol_type="genomic DNA"
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REFERENCE	1	(bases 1 to 901)
AUTHORS	Berezikov, B., Guryev, V., van de Belt, J., Wienholds, E., Plasterk, R.H. and Cuppen, E.	
TITLE	Phylogenetic Shadowing and Computational Identification of Human microRNA Genes	
JOURNAL	Cell 120 (1), 21-24 (2005)	
PUBLISHED	1565478	
REFERENCE	2	(bases 1 to 901)
AUTHORS	Berezikov, B., Guryev, V., van de Belt, J., Wienholds, E., Plasterk, R.H.A. and Cuppen, E.	
TITLE	Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaan 8, Utrecht	
JOURNAL	3584 CT, The Netherlands	
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Best Local Similarity		73.5%; Pred. No. 1.6e-20;
Matches		61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
QY	1	CCUTUGAGAUAGAUGAGCACAUAAUGCGUUGUGAUATUGAAAGGUGAGGCCAUU 60
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QY	61	UGUGCCGCUCAAAUACAGG 83
Db	522	TGTCCTGCCTCAAATAACAGG 544
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LOCUS		AY866303
DEFINITION		Pan paniscus microRNA mir-15a and microRNA mir-16-1 genes, complete sequence.
ACCESSION		AY866303
VERSION		AY866303.1
KEYWORDS		
SOURCE		.
ORGANISM		Pan paniscus (pygmy chimpanzee)
REFERENCE		Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
AUTHORS		1 (bases 1 to 914) Berezikov, B., Guryev, V., van de Belt, J., Wienholds, E., Plasterk, R.H. and Cuppen, E.
TITLE		Phylogenetic Shadowing and Computational Identification of Human microRNA Genes
JOURNAL		Cell 120 (1), 21-24 (2005)
PUBLISHED		15652478
REFERENCE	2	(bases 1 to 914)
AUTHORS	Berezikov, B., Guryev, V., van de Belt, J., Wienholds, E., Plasterk, R.H.A. and Cuppen, E.	
TITLE	Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaan 8, Utrecht	
JOURNAL	3584 CT, The Netherlands	
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Matches		61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
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Oy	61	UGUGUGCCUCAAAUACAGG	83	Homo sapiens chromosome 13q14 BAC clone CIRB-369L16, complete sequence.
Db	535	TGTGCTGCCTCAAAATACAGG	557	AF334404.1 GI:13507269
RESULT 13				
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DEFINITION	Homo sapiens chromosome 13 clone 317g11 map 13q14, complete sequence.	PRI	09-APR-2003	
ACCESSION	AC069475			
VERSION	AC069475.27	GI:11992970		
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
TITLE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buttheria; Euarchoptoglires; Primates; Catarrhini; Homidae; Homo.			
REFERENCE	1 (bases 1 to 153092)			
AUTHORS	Malai,E., Cowell,J.K. and Roe,B.A.			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 153092)			
AUTHORS	Malai,E., Cowell,J.K. and Roe,B.A.			
JOURNAL	Direct Submission			
REFERENCE	3 (bases 1 to 153092)			
AUTHORS	Malai,E., Cowell,J.K. and Roe,B.A.			
JOURNAL	Submitted (01-JUN-2000) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA			
REFERENCE	4 (bases 1 to 153092)			
AUTHORS	Malai,E., Cowell,J.K. and Roe,B.A.			
JOURNAL	Direct Submission			
REFERENCE	-----			
AUTHORS	-----			
JOURNAL	Submitted (27-DEC-2000) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA			
COMMENT	On Dec 27, 2000 this sequence version replaced gi:11560201.			
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	/organism="Homo sapiens"			
	/mol_type="genomic DNA"			
	/db_xref="txon:9606"			
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	/clone="317g11"			
ORIGIN				
	Query Match	100.0%	Score 83;	DB 5;
	Best Local Similarity	73.5%;	Pred. No. 2.2e-20;	Length 153092;
	Matches	61;	Conservative	Mismatches 0;
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Oy	61	UGUGUGCCUCAAAUACAGG	83	Homo sapiens chromosome 13q14 BAC clone CIRB-369L16, complete sequence.
Db	376	TGTGCTGCCTCAAAATACAGG	354	AF334404.1 GI:13507269
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	Matches	61;	Conservative	Mismatches 0;
	Indels	0;	Gaps 0;	
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Oy	61	UGUGUGCCUCAAAUACAGG	83	Homo sapiens chromosome 13q14 BAC clone CIRB-369L16, complete sequence.
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AL37060/c
 LOCUS AL137060 154887 bp DNA linear PR1 18-MAY-2005
 DEFINITION Human DNA sequence from clone RP11-34F20 on chromosome 13. Contains the 3' end of the RFP2 gene for ret finger protein 2, the DLEU2 gene for deleted in lymphocytic leukemia 2 (LCMSUN), the 5' end of the DLEU1 gene for deleted in lymphocytic leukemia 1 (LCMSUN), a ribosomal protein L18 (RPL18) pseudogene, a novel gene and four CPG islands, complete sequence.
 ACCESSION AL137060
 VERSION AL137060.13 GI:1120982
 KEYWORDS HUG; BCMS; BCMS; CPG Island; DLEU1; DLEU2; LEU1; LEU2; Lymphocytic Leukemia; RFP2; RPL18.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 154887)
 REFERENCE Pearce, A.
 AUTHORS Pearce, A.
 TITLE Direct Submission
 JOURNAL Submitted [13-MAY-2005] Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
 COMMENT The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPBP; Information on the WORMBP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormbp This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chromosome_13/RP11-34F20 is from the library RPCL-11.1 constructed by the group of Pieten de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACe3.6

 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: vega@sanger.ac.uk

 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

 FEATURES
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Best Local Similarity 73.5%; Pred. No. 2.2e-20; Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

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Db 42660 CCTTGGAGTAAGTAGGAGACATAATGGTTGGGTTTGAAGGTCAGGCCAT 42601
Qy 61 UGUGCGGCCGAAAAUACAGG 83
Db 42600 TGTGCGCCCTCAAATACAAAGG 42576

Search completed: November 1, 2006, 20:59:43
Job time : 1838.86 secs

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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 19:02:55 ; Search time 397.61 Seconds
(without alignments)
1455.440 Million cell updates/sec

Title: US-10-706-798-1

Perfect score: 83

Sequence: 1 ccuugagguaaagugcagg.....gcugccucaaaauacaagg 83

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq 8;*

- 1: geneseqn1980s;*
- 2: geneseqn1990s;*
- 3: geneseqn2000s;*
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- 5: geneseqn2001bs;*
- 6: geneseqn2002as;*
- 7: geneseqn2002bs;*
- 8: geneseqn2003as;*
- 9: geneseqn2003bs;*
- 10: geneseqn2003cs;*
- 11: geneseqn2003ds;*
- 12: geneseqn2004as;*
- 13: geneseqn2004bs;*
- 14: geneseqn2005as;*
- 15: geneseqn2006s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

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4	83	100.0	14	AED35990 Human mir	
5	83	100.0	15	AEB26703 Hsa miR-1	
6	83	100.0	15	AEE99350 Human mir	
7	83	100.0	14	Ado17089 Human gen	
8	82	98.8	4	AAK72317 Human gen	
9	80	96.4	110	Ado30345 Human pri	
10	79	95.6	14	Ado303080 Human pri	
11	68	82.7	108	AEB2619 Human pri	
12	61.8	74.5	14	Ado04205 Mouse pri	
13	40	48.2	14	AEB92912 Human mir	
14	40	48.2	14	AEB92913 Human mir	
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C	16	33.4	40.2	14	AEB92620 Human mir
C	17	33.4	40.2	83	AED35990 Human mir
C	18	33.4	40.2	15	AEE99350 Human mir

SUMMARIES

Result No.	Score	Match Length	DB ID	Description	
1	83	100.0	83	Ado17089 Human mir	
2	83	100.0	12	Ado17089 Human mir	
3	83	100.0	14	AEB2620 Human mir	
4	83	100.0	14	AED35990 Human mir	
5	83	100.0	15	AEB26703 Hsa miR-1	
6	83	100.0	15	AEE99350 Human mir	
7	83	100.0	14	Ado17089 Human gen	
8	82	98.8	4	AAK72317 Human gen	
9	80	96.4	110	Ado30345 Human pri	
10	79	95.6	14	Ado303080 Human pri	
11	68	82.7	108	AEB2619 Human pri	
12	61.8	74.5	14	Ado04205 Mouse pri	
13	40	48.2	14	AEB92912 Human mir	
14	40	48.2	14	AEB92913 Human mir	
C	15	33.4	40.2	12	Ado17089 Human mir
C	16	33.4	40.2	14	AEB92620 Human mir
C	17	33.4	40.2	83	AED35990 Human mir
C	18	33.4	40.2	15	AEE99350 Human mir

ALIGMENTS

Result No.	Score	Match Length	DB ID	Description	
1	83	100.0	83	Ado17089 Human mir	
2	83	100.0	12	Ado17089 Human mir	
3	83	100.0	14	AEB2620 Human mir	
4	83	100.0	14	AED35990 Human mir	
5	83	100.0	15	AEB26703 Hsa miR-1	
6	83	100.0	15	AEE99350 Human mir	
7	83	100.0	14	Ado17089 Human gen	
8	82	98.8	4	AAK72317 Human gen	
9	80	96.4	110	Ado30345 Human pri	
10	79	95.6	14	Ado303080 Human pri	
11	68	82.7	108	AEB2619 Human pri	
12	61.8	74.5	14	Ado04205 Mouse pri	
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14	40	48.2	14	AEB92913 Human mir	
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C	16	33.4	40.2	14	AEB92620 Human mir
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 XX PD 27-MAY-2004.
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 XX PF 12-NOV-2003; 2003WO-US035777.
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 XX PR 13-NOV-2002; 2002US-0425864P.
 PR 09-MAY-2003; 2003US-0469464P.
 XX PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Croce CM, Calin GA;
 XX DR WPI; 2004-400825/37.
 XX
 PT Treating an miR15 or miR16 mediated cancer, i.e. chronic lymphocytic
 PT leukemia or prostate cancer, comprises administering to the subject an
 PT miR15 or miR16 gene product.
 XX
 PT Claim 64; SEQ ID NO 1; 73pp; English.
 XX
 CC This invention relates to a novel method of treating an miR15 or miR16
 CC mediated cancer in a subject which comprises administering to the subject
 CC an amount of an isolated miR15 or miR16 gene product such that
 CC proliferation of miR15 or miR16 mediated cancer cells is inhibited. The
 CC miR15 and miR16 micro RNA genes are localised to 1q14 in humans, a
 CC region that is deleted in a significant portion of subjects suffering
 CC from chronic lymphocytic leukaemia or prostate cancer. The products of
 CC the miR15 and miR16 genes have also been found to inhibit the neoplastic
 CC or tumourigenic growth of chronic lymphocytic leukaemia or prostate
 CC cancer cells. The invention may be useful for the production of compounds
 CC with a cytotoxic activity. In addition the invention may also be useful
 CC for gene therapy using the miR15 or miR16 gene product. The methods and
 CC compositions are useful in diagnosing and treating miR15 or miR16
 CC mediated cancer, i.e. chronic lymphocytic leukaemia or prostate cancer.
 CC The present sequence is that of the human miR15 precursor RNA sequence
 CC which is used in the method of the invention.
 XX
 SQ Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;
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 Best Local Similarity 100.0%; Pred. No. 2.1e-20; Mismatches 0; Indels 0; Gaps 0;
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 Db 61 UGGUGUGGCCAAGAACAGGG 83
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 ID ABB92620 standard; DNA; 83 BP.

XX AC ABB92620;
 XX DT 03-NOV-2005 (first entry)
 XX DE Human microRNA gene SEQ ID NO 33.
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 XX KW cytostatic; gene therapy; diagnosis; prognosis; pharmaceutical;
 KW gene expression; musculoskeletal disease; hematological disease;
 KW immunostimulant; andrology; neurological disease; dermatological disease;
 KW endocrine disease; gynecology and obstetrics; respiratory disease;
 KW gastrointestinal disease; genitourinary disease; cancer; neoplasm;
 KW microRNA; miR; ss; biochip.
 OS Homo sapiens.
 XX
 PN WO2005078139-A2.
 XX
 XX PD 25-AUG-2005.
 XX
 XX PF 09-FEB-2005; 2005WO-US004865.
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 XX PR 09-FEB-2004; 2004US-0542939P.
 PR 03-FEB-2004; 2004US-0542940P.
 PR 09-FEB-2004; 2004US-0542939P.
 PR 09-FEB-2004; 2004US-0543119P.
 PR 18-JUN-2004; 2004US-0580797P.
 PR 18-JUN-2004; 2004US-0580959P.
 XX PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Croce CM, Liu C, Calin GA;
 XX DR WPI; 2005-571622/58.
 XX
 PT Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer,
 PT tumors, or myelodysplastic syndrome, comprises evaluating a miR gene in
 PT the test sample.
 XX
 PS Example 1; SEQ ID NO 33; 170pp; English.
 XX
 CC The invention describes diagnosing whether a subject has, or is at risk
 CC for developing, a cancer linked to a cancer-associated chromosomal
 CC feature, comprises evaluating the status of at least one
 CC microRNA (miR) gene located in close proximity to the cancer-associated
 CC chromosomal feature. Also described are a pharmaceutical composition
 CC comprising an isolated miR gene product or a nucleic acid encoding an
 CC isolated miR gene product from an miR gene located in close proximity to
 CC a cancer-associated chromosomal feature and is not miR15 or miR16, and a
 CC pharmaceutical carrier; and a method of treating cancer associated with a
 CC cancer-associated chromosomal feature in a subject. The miR, composition,
 CC and method are useful for diagnosing and treating a cancer-associated
 CC chromosomal feature, where the cancer is bladder cancer, esophageal
 CC cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer,
 CC ovarian cancer, breast cancer, lymphoma, Ewing's sarcoma, hematopoietic
 CC tumors, solid tumors, gastric cancer, colorectal cancer, brain cancer,
 CC epithelial cancer, nasopharyngeal cancer, uterine cancer, hepatic cancer,
 CC head-and-neck cancer, renal cancer, male germ cell tumors, malignant
 CC mesothelioma, myelodysplastic syndrome, pancreatic or biliary cancer, Wilms'
 CC prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilms' tumor, small cell lung cancer, melanoma, skin cancer, osteosarcoma,
 CC neuroblastoma, leukemia, acute lymphocytic leukemia, acute myeloid
 CC leukemia, chronic lymphocytic leukemia, glioblastoma multiforme,
 CC medulloblastoma, lymphoplasmacytoid lymphoma, rhabdomyosarcoma, B-cell
 CC chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia
 CC associated with an unmutated *IGHM* gene, *ZAP-70* expression, *CD38*
 CC expression, a deletion at chromosome 1q33, a loss or mutation of *TP53* or
 CC their combination. This sequence represents a human microRNA (miRNA)
 CC gene.
 XX
 SQ Sequence 83 BP; 26 A; 13 C; 22 G; 22 T; 0 U; 0 Other;
 Query Match 100.0%; Score 83; DB 14; Length 83;

Best Local Similarity 73.5%; Pred. No. 2.1e-20; Mismatches 0; Indels 0; Gaps 0; Matches 61; Conservative 22;

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 1 CCTUGGAGUAAUGAGCACAUAAUGUGAAGUGGAGCCAUU 60
 Qy 61 ugugcucuccaaaaaacagg 83
 61 TGTGCTGCCTCAAAATACAGG 83

Db AED35990;
 AC AED35990;
 XX DT 15-DEC-2005 (first entry)
 DB Human micro RNA miR-15a precursor.
 XX KW RNA interference; RNA purification; RNA amplification; gene silencing;
 KW RNA detection; micro RNA; miRNA; miR-15a; ss.
 XX OS Homo sapiens.
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 FT /note= "Corresponds to mature miRNA"

W02005098029-A2.

XX PD 20-OCT-2005.
 XX PP 07-APR-2005; 2005WO-DK000239.
 XX PR 07-APR-2004; 2004DK-00000578.
 PR 23-JUL-2004; 2004DK-00001146.
 PR 11-AUG-2004; 2004DK-00001218.
 PR 15-OCT-2004; 2004DK-00001587.
 PR 28-JAN-2005; 2005DK-00000140.
 XX PA (EXIQ-) EXIQON AS.
 XX PI Jacobsen N, Kongsbak L, Kauppinen S, Schwald SM, Mouritzen P;
 PT Nielsen PS, Norholm M;
 XX DR WPI; 2005-714540/73.

PT Isolating, purifying, amplifying, detecting, identifying, quantifying or capturing non-coding RNAs such as micro RNA or small interfering RNA (siRNA), involves using oligonucleotide containing nucleoside analogs.

RS Disclosure; Fig 29; 10pp; English.

CC The present invention relates to the use of an oligonucleotide for the isolation, purification, amplification, detection, identification, quantification or capture of microRNA (miRNA) or small interfering RNA (siRNA), where the oligonucleotide contains a number of nucleoside analogs. The method uses 2 anchored tagging probes, each designed in combination to detect a complementary target sequence, e.g. a short RNA sequence, where the first tagging probe hybridizes to a first region within a target sequence and the second tagging probe hybridizes to a second region within the same complementary target sequence, e.g. a short RNA target sequence that is adjacent to the first region. In a preferred mode, one of the tagging probes is 5' phosphorylated to enable covalent coupling of the 2 contiguous tagging probes hybridized to the complementary target sequence by a ligase to form a single oligonucleotide sequence. The method takes advantage of substitution of

CC the recognition sequences with high-affinity nucleotide analogs, e.g. locked nucleic acid (LNA), for sensitive and specific hybridization to short target sequences, e.g. mRNAs or siRNAs. The ligation reaction is followed by real-time quantitative PCR (qPCR) of the target sequence, e.g. ribonucleic acid-templated, covalently joined oligonucleotide molecules using anchor sequences attached to the tagging probes as priming sites for the PCR primers and a short detection probe with sufficient duplex stability to allow binding to the amplicon, and employing any of a variety of detection principles used in homogeneous assays. In the preferred mode, the detection probe is substituted with duplex-stabilizing, high-affinity nucleotide analogs, e.g. LNA, and preferably oxy-LNA, to allow the use of short detection probe in the real-time qPCR. The method is useful for detecting and quantifying individual small RNA molecules in complex mixtures of different nucleic acids, and for detecting, testing, diagnosing or quantifying miRNAs, siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative mRNA splice variants implicated in, or connected to, human disease in complex nucleic acid samples, e.g. from cancer patients. The present sequence is that of human mRNA Hsa miR-15a precursor. miR-15a AED35991 was used as the target in examples from the invention.

SQ Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;

Query Match 100.0%; Score 83; DB 14; Length 83;
 Best Local Similarity 100.0%; Pred. No. 2.1e-20; Mismatches 0; Indels 0; Gaps 0; Matches 83; Conservative 0;

Qy 1 CCTUGGAGUAAUGAGCACAUAAUGUGAAGUGGAGCCAUU 60
 1 CCTUGGAGUAAUGAGCACAUAAUGUGAAGUGGAGCCAUU 60
 Qy 61 ugugcucuccaaaaaacagg 83
 61 ugugcucuccaaaaaacagg 83

Db ABB26703;
 AC ABB26703;
 XX DT 09-FEB-2006 (first entry)
 XX DB Hsa miR-15a precursor sequence, SEQ ID 72.
 XX KW RNA amplification; RNA detection; RNA purification; miRNA; microRNA; ss.
 XX OS Synthetic.

XX FH Key location/Qualifiers
 FT misc_binding 1. .5 /*tag= a
 FT misc_binding 13. .5 /*tag= b
 FT misc_binding 16. .23 /*tag= c
 FT misc_binding 38. .39 /*tag= e
 FT misc_binding 26. .35 /*tag= d
 FT misc_binding 45. .46 /*tag= f
 FT misc_binding

/bound_moiety= "Nucleotides 68. .61 of the present sequence"
 /bound_moiety= "Nucleotides 46. .45 of the present sequence"
 /bound_moiety= "Nucleotides 58. .49 of the present sequence"
 /bound_moiety= "Nucleotides 39. .38 of the present sequence"

FT sequence"
 FT 49. .58
 FT /*tag= g
 FT /bound_moiety= "Nucleotides 35. .26 of the present
 FT sequence"
 FT 61. .68
 FT /*tag= h
 FT /bound_moiety= "Nucleotides 23. .16 of the present
 FT sequence"
 FT 71.
 FT /*tag= i
 FT /bound_moiety= "Nucleotide 13 of the present sequence"
 FT 79. .83
 FT /*tag= j
 FT /bound_moiety= "Nucleotides 5. .1 of the present sequence"
 XX US2005272075-A1.
 XX PD 08-DEC-2005.
 XX PR 07-APR-2005; 2005US-0100897.
 XX PR 07-APR-2004; 2004US-0560148P.
 PR 13-JUL-2004; 2004US-0600961P.
 PR 15-OCT-2004; 2004US-0619291P.
 PR 28-JAN-2005; 2005US-0648221P.
 XX PA (UKC/) JACOBSEN N.
 PA (KONG/) KONGBAK L.
 PA (KAUP/) KAUPPINEN S.
 PA (ECHW/) ECHWALD S. M.
 PA (MOUR/) MOURITZEN P.
 PA (INTEL/) NIELSEN P. S.
 PA (NORTH/) NORHOLM M.
 XX PI Jacobsen N, Kongbak L, Kauppinen S, Echwald SM, Mouritzen P;
 PI Nielsen PS, Norholm M;
 XX DR WPI; 2006-037202/04.
 XX PT Isolating, purifying, amplifying, detecting identifying, quantifying, or
 PT capturing non-coding RNAs, such as microRNA or small interfering RNA
 PT (siRNA) by using an oligonucleotide containing a number of nucleoside
 PT analogues.
 XX Disclosure; SEQ ID NO 72; 113pp; English.
 The present invention relates to novel methods for quantifying non-coding
 RNAs, such as microRNA or short interfering RNA (siRNA). The methods
 comprises using an oligonucleotide containing a number of nucleoside
 analogues e.g. LNA analogues. The methods are useful for detecting and
 quantifying individual small RNA molecules in complex mixtures composed
 of hundreds of thousands of different nucleic acids. The present sequence
 was used to illustrate the invention.
 XX Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;
 SQ Query Match Best Local Similarity 100.0%; Score 83; DB 15; Length 83;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTUGGAGUAGAGUGCAGCACAUAGGUUGUGGAUTTUGAAAGGUCCAGGCCAUU 60
 Db 1 CCTUGGAGUAGAGUGCAGCACAUAGGUUGUGGAUTTUGAAAGGUCCAGGCCAUU 60
 QY 61 UGUGUGGCCUCAAAUACAGG 83
 Db 61 UGUGUGGCCUCAAAUACAGG 83
 RESULT 5 AEB9350

ID AEB9350 standard; RNA; 83 BP.
 XX AC AEB9350;
 XX DT 23-FEB-2006 (first entry)
 XX DB Human miRNA sequence, hsa-mir-15a.
 XX KW RNA detection; microarray; diagnosis; genetic marker; drug screening; SB.
 XX OS Homo sapiens.
 XX PN W02005118806-A2.
 XX PD 15-DEC-2005.
 XX PR 31-MAY-2005; 2005WO-US018826.
 XX PR 28-MAY-2004; 2004US-0575743P.
 PR 03-FEB-2005; 2005US-0649584P.
 XX PA (AMBI-) AMBITION INC.
 XX PI Brown D, Conrad R, Devroe E, Goldrick M, Keiger K, Labourier E;
 PI Moon I, Powers P, Shelton J, Shingara J;
 XX DR Moon I, Powers P, Shelton J, Shingara J;
 XX WPI; 2006-047544/05.
 CC Multi-labeling miRNA in a sample, by forming a reaction mixture for
 PT enzyme catalysis, where tailed miRNA molecules are produced, and
 PT attaching a label to the tailed miRNA molecules.
 XX Disclosure; SEQ ID NO 22; 307pp; English.
 The new invention relates to manipulation of miRNA and their use in
 characterizing their role and function in cells. Described is a method of
 multi-labeling miRNA in a sample by forming a reaction mixture for enzyme
 catalysis, comprising the miRNA with an enzyme that catalyzes the
 addition of di- or tri-phosphate nucleotides, and one or more labeled or
 unlabeled nucleotides, where tailed miRNA molecules are produced; and
 attaching a label to the tailed miRNA molecules. Specifically, the method
 comprises enriching miRNA in the sample; forming a reaction mixture,
 under conditions that allows enzyme catalysis, where tailed miRNA
 molecules are produced; and if unlabeled nucleotides are added to the
 miRNA, attaching a label to the tailed miRNA molecules. Also given
 include a miRNA array comprising one or more miRNA probes immobilized on
 a solid support, where the probes comprise an miRNA coding sequence, and
 an amine attached to the 5' or 3' end of the probe; evaluating miRNA in a
 sample; identifying a correlation between miRNA expression and a disease
 or condition; analyzing miRNA in a sample, identifying a candidate
 diagnostic marker or therapeutic target of a disease or condition;
 determining a difference between two or more biological samples;
 screening for a candidate therapeutic agent for a disease or condition;
 and a kit for preparing miRNA for multi-labeling. The methods and
 compositions are useful for isolating, enriching, and/or labeling miRNA
 molecule samples. The present sequence is a human miRNA sequence, used in
 the new methods of the invention.
 XX Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;
 SQ Query Match Best Local Similarity 100.0%; Score 83; DB 15; Length 83;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTUGGAGUAGAGUGCAGCACAUAGGUUGUGGAUTTUGAAAGGUCCAGGCCAUU 60
 Db 1 CCTUGGAGUAGAGUGCAGCACAUAGGUUGUGGAUTTUGAAAGGUCCAGGCCAUU 60
 QY 61 UGUGUGGCCUCAAAUACAGG 83
 Db 61 UGUGUGGCCUCAAAUACAGG 83
 RESULT 5 AEB9350

PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 22-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0231414P.
 PR 06-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 21-SEP-2000; 2000US-0234997P.
 PR 21-SEP-2000; 2000US-0235484P.
 PR 21-SEP-2000; 2000US-0235834P.
 PR 21-SEP-2000; 2000US-0235836P.
 PR 21-SEP-2000; 2000US-0236327P.
 PR 21-SEP-2000; 2000US-0236367P.
 PR 21-SEP-2000; 2000US-0236369P.
 PR 21-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.

PR 03-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246699P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249219P.
 PR 17-NOV-2000; 2000US-0249220P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 03-DEC-2000; 2000US-0251030P.
 PR 03-DEC-2000; 2000US-0249225P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 05-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251836P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251889P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Barash SC, Ruben SM;

XX DR WPI: 2001-483426/52.

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

XX Disclosure; SEQ ID NO 27129; 3071PP + Sequence Listing; English.

XX AAK54951 to AAK67102 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAW82170 to AAW9121. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK6703 to AAK8764 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAW82169 represent sequences used in the exemplification of the present invention

CC medulloblastoma, lymphoplasmacytoid lymphoma, rhabdomyosarcoma, B-cell
 CC chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia
 CC associated with an unimutated IgH gene, ZAP-70 expression, CD88 expression, a deletion at chromosome 11q23, a loss or mutation of TP53 or
 CC their combination. This sequence represents a human microRNA (miRNA)
 CC gene.
 XX Sequence 108 BP; 38 A; 15 C; 26 G; 29 T; 0 U; 0 Other;
 SQ
 Query Match 95.2%; Score 79; DB 14; Length 108;
 Best Local Similarity 72.2%; Pred. No. 6.7e-19; Matches 57; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
 AC AEE99543;
 XX
 AC AEE99543;
 XX
 DT 23-FEB-2006 (first entry)
 XX
 DE Mouse miRNA sequence, mmu-mir-15a.
 XX RNA detection; microarray; diagnosis; genetic marker; drug screening; ss.
 XX OS Mus musculus.
 XX PN WO2005118806-A2.
 XX PD 15-DEC-2005.
 XX PF 31-MAY-2005; 2005WO-US018826.
 XX PR 28-MAY-2004; 2004US-0375743P.
 XX PR 03-FEB-2005; 2005US-0649584P.
 XX PA (AMBI-) AMBION INC.
 XX PI Brown D, Conrad R, Devroe E, Goldrick M, Keiger K, Labourier E;
 PI Moon I, Powers P, Shelton J, Shingara J;
 DR XX WPI; 2006-047544/05.
 XX PT Multi-labeling miRNA in a sample, by forming a reaction mixture for
 PT enzyme catalysis, where tailed miRNA molecules are produced, and
 PT attaching a label to the tailed miRNA molecules.
 XX Disclosure; SEQ ID NO 215; 307pp; English.
 CC The new invention relates to manipulation of miRNA and their use in
 CC characterizing their role and function in cells. Described is a method of
 CC multi-labeling miRNA in a sample by forming a reaction mixture for enzyme
 CC catalysis, comprising the miRNA with an enzyme that catalyzes the
 CC addition of di- or tri-phosphate nucleotides, and one or more labeled or
 CC unlabeled nucleotides, where tailed miRNA molecules are produced; and
 CC attaching a label to the tailed miRNA molecules. Specifically, the method
 CC comprises enriching miRNA in the sample; forming a reaction mixture,
 CC under conditions that allows enzyme catalysis, where tailed miRNA
 CC molecules are produced; and if unlabeled nucleotides are added to the
 CC miRNA, attaching a label to the tailed miRNA molecules. Also given
 CC include a miRNA array comprising one or more miRNA probes immobilized on
 CC a solid support, where the probes comprise an miRNA coding sequence, and
 CC an amine attached to the 5 or 3' end of the probe; evaluating miRNA in a
 sample; identifying a correlation between miRNA expression and a disease

CC or condition; analyzing miRNA in a sample; identifying a candidate
 CC diagnostic marker or therapeutic target of a disease or condition;
 CC determining a difference between two or more biological samples;
 CC screening for a candidate therapeutic agent for a disease or condition;
 CC and a kit for preparing miRNA for multi-labeling. The methods and
 CC compositions are useful for isolating, enriching, and/or labeling miRNA
 CC molecule samples. The present sequence is a mouse miRNA sequence, used in
 XX the new methods of the invention.
 SQ Sequence 83 BP; 26 A; 15 C; 22 G; 0 T; 20 U; 0 Other;
 XX
 Query Match 82.7%; Score 68.6; DB 15; Length 83;
 Best Local Similarity 94.7%; Pred. No. 4.1e-15; Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 AC QY 1 CCTUGGAGTAAGUAGCAGCACAUAAUGAUUUGGATUTUGAAGGUGCAGCCAUAU 60
 AC Db 30 CCTTGAGGAAAGTAGCAGCACATAATGGTTGGATTTGAAAGGGCAGCCATAT 89
 AC QY 61 UGGUGUGCCUCAAAAUAC 79
 AC Db 90 TGTGCTGCCCTCAAAATAAC 108
 XX
 RESULT 11
 AC AEE99543
 ID AEE99543 standard; RNA; 83 BP.
 XX
 AC AEE99543;
 XX
 AC AEE99543;
 XX
 DT 23-FEB-2006 (first entry)
 XX
 DE Mouse miRNA sequence, mmu-mir-15a.
 XX RNA detection; microarray; diagnosis; genetic marker; drug screening; ss.
 XX OS Mus musculus.
 XX PN WO2005118806-A2.
 XX PD 15-DEC-2005.
 XX PF 31-MAY-2005; 2005WO-US018826.
 XX PR 28-MAY-2004; 2004US-0375743P.
 XX PR 03-FEB-2005; 2005US-0649584P.
 XX PA (AMBI-) AMBION INC.
 XX PI Brown D, Conrad R, Devroe E, Goldrick M, Keiger K, Labourier E;
 PI Moon I, Powers P, Shelton J, Shingara J;
 DR XX WPI; 2006-047544/05.
 XX PT Multi-labeling miRNA in a sample, by forming a reaction mixture for
 PT enzyme catalysis, where tailed miRNA molecules are produced, and
 PT attaching a label to the tailed miRNA molecules.
 XX Disclosure; SEQ ID NO 215; 307pp; English.
 CC The new invention relates to manipulation of miRNA and their use in
 CC characterizing their role and function in cells. Described is a method of
 CC multi-labeling miRNA in a sample by forming a reaction mixture for enzyme
 CC catalysis, comprising the miRNA with an enzyme that catalyzes the
 CC addition of di- or tri-phosphate nucleotides, and one or more labeled or
 CC unlabeled nucleotides, where tailed miRNA molecules are produced; and
 CC attaching a label to the tailed miRNA molecules. Specifically, the method
 CC comprises enriching miRNA in the sample; forming a reaction mixture,
 CC under conditions that allows enzyme catalysis, where tailed miRNA
 CC molecules are produced; and if unlabeled nucleotides are added to the
 CC miRNA, attaching a label to the tailed miRNA molecules. Also given
 CC include a miRNA array comprising one or more miRNA probes immobilized on
 CC a solid support, where the probes comprise an miRNA coding sequence, and
 CC an amine attached to the 5 or 3' end of the probe; evaluating miRNA in a
 sample; identifying a correlation between miRNA expression and a disease

CC or condition; analyzing miRNA in a sample; identifying a candidate
 CC diagnostic marker or therapeutic target of a disease or condition;
 CC determining a difference between two or more biological samples;
 CC screening for a candidate therapeutic agent for a disease or condition;
 CC and a kit for preparing miRNA for multi-labeling. The methods and
 CC compositions are useful for isolating, enriching, and/or labeling miRNA
 CC molecule samples. The present sequence is a mouse miRNA sequence, used in
 XX the new methods of the invention.

Query Match 82.7%; Score 68.6; DB 15; Length 83;
 Best Local Similarity 94.7%; Pred. No. 4.1e-15; Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 AC QY 1 CCTUGGAGTAAGUAGCAGCACAUAAUGAUUUGGATUTUGAAGGUGCAGGCCAUAU 60
 AC Db 1 CCTUGGAGTAAGUAGCAGCACATAATGGTTGGATTTGAAAGGGCAGCCATAT 89
 AC QY 61 UGGUGUGCCUCAAAAUAC 79
 AC Db 61 UGGUGUGCCUCAAAAUAC 75
 XX
 RESULT 12
 AC A0X04205
 ID A0X04205 standard; RNA; 70 BP.
 XX
 AC A0X04205;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Mouse primary-miRNA (pri-miRNA) mir-15a.
 XX
 KW MiRNA; ds; RNA interference; gene silencing; Cytostatic; Antidiabetic;
 KW Antorectic; Antilipemic; Antiarrhoic; Hypotensive;
 KW Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
 KW Rating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
 KW angiogenesis disorder; cardiovascular disease;
 KW non-insulin dependent diabetes; endocrine disease;
 KW gastrointestinal disease; metabolic disorder; obesity;
 KW nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
 KW hypertension; anorexia nervosa; nutritional disorder;
 KW psychiatric disorder; Alzheimer's disease; degeneration;
 KW neurological disease; nervous system injury; neurodegenerative disease;
 KW neurological disorder.
 XX
 OS Mus sp.
 XX PN WO2005113901-A2.
 XX PD 17-FEB-2005.
 XX PF 30-JUL-2004; 2004WO-US025300.
 XX PR 31-JUL-2003; 2003US-0492056P.
 XX PR 31-OCT-2003; 2003US-0516303P.
 XX PR 19-DEC-2003; 2003US-0531596P.
 XX PR 14-APR-2004; 2004US-0562417P.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Ebau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF;
 PI Vickers T, Marcusson EG, Koller E, Swayze BE, Jain R, Bhat B;
 PI Peralta E;
 XX DR WPI; 2005-163123/17.
 XX PT New oligomeric compound that can hybridize with or sterically interfere
 PT with nucleic acid molecules comprising or encoding small non-coding RNA
 PT targets, useful for treating e.g., cancer and diabetes.
 XX PS Example 34; SEQ ID NO 1316; 854pp; English.

CC XX The invention relates to an oligomeric compound comprising a first region
 CC and a second region, where at least one region contains a modification,
 CC and a portion of the oligomeric compound is targeted to a small non-
 CC coding RNA target nucleic acid that is miRNA (micro-RNA), or its
 CC precursor (primary-miRNA, pri-miRNA). Also included are a composition
 CC comprising a first oligomeric compound and a second oligomeric compound
 (where at least one of the oligomeric compounds contains a modification),
 CC at least a portion of the first oligomeric compound is capable of
 CC hybridizing with at least a portion of the second oligomeric compound,
 CC and at least a portion of the first oligomeric compound is targeted to a
 CC small non-coding RNA target nucleic acid, a pharmaceutical composition
 CC comprising the composition cited above (and a carrier), a kit or assay
 CC device comprising the composition, modulating the expression of a small
 CC non-coding RNA target nucleic acid in a cell (or tissue or animal),
 CC treating or preventing a disease or disorder associated with a small non-
 CC coding RNA target nucleic acid, treating a condition in an animal,
 CC treating or preventing a disease or disorder associated with an animal,
 CC methods of screening an oligomeric compound for an effect on miRNA
 CC signaling, methods of modulating translation (or apoptosis, conversion of
 CC a precursor miRNA into miRNA, or cellular differentiation), identifying
 CC an RNA transcript bound to a small non-coding RNA, arresting (or
 CC delaying) entry of a cell at the G2/M phase, interfering with chromosome
 CC segregation, a method of triggering apoptosis, detecting a miRNA
 CC precursor, identifying a miRNA target, modulating cellular
 CC differentiation, treating a condition associated with adipocyte
 CC differentiation in an animal, treating/preventing a disease/disorder
 CC associated with aberrant regulation of the cell cycle by miRNAs,
 CC maintaining a pluripotent stem cell and identifying a small non-coding
 CC RNA binding site. The oligomeric compound is targeted to a region
 CC flanking a prokra cleavage site within a pri-miRNA. It stimulates an
 CC increase in expression of a pri-miRNA. The compounds and compositions are
 CC useful for treating a disease or disorder resulting from chromosomal non-
 CC disjunction, altered methylation, acetylation, or pseudouridylation state
 CC of chromosome, such as a hyperproliferative condition (e.g. cancer,
 CC neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
 CC hyperlipidemia, atherosclerosis, hypertension, anorexia,
 CC Alzheimer's disease, a central nervous system injury or neurodegenerative
 CC disorder. The present sequence is a primary miRNA of the invention.
 XX

SQ Sequence 70 BP; 23 A; 12 C; 18 G; 0 T; 17 U; 0 Other;
 Query Match 74.5%; Score 61.8; DB 14; Length 70;
 Best Local Similarity 96.9%; Pred. No. 1.2e-12;
 Matches 63; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 AGUGGAGGACAUAAUGGUUGUGGAUUUGAAAGGUCCAGGCCAUAAUGGUCCUGGU 70
 Db 1 AAUGUNGAGGACAUAAUGGUUGUGGAUUGAAAGGUCCAGGCCAUACUGUGCUGGU 60

QY 71 CAAA 75

Db 61 CAAA 65

RESULT 13

SQ Sequence 40 BP; 11 A; 5 C; 11 G; 13 T; 0 U; 0 Other;
 AEB92912 48.2%; Score 40; DB 14; Length 40;
 ID Best Local Similarity 67.5%; Pred. No. 0.00011;
 AC Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX DT 03-NOV-2005 (first entry)

DE Human microRNA gene probe SEQ ID NO 325.

XX

KW cytostatic; gene therapy; diagnosis; prognosis; pharmaceutical;
 KW gene expression; musculoskeletal disease; hematological disease;
 KW immunostimulant; andrology; neurological disease; dermatological disease;
 KW endocrine disease; gynecology and obstetrics; respiratory disease;
 KW gastrointestinal disease; genitourinary disease; cancer; neoplasm;
 KW microRNA; miR; ss; bichip; probe.

XX

OS Homo sapiens.
 XX PN WO2005078139-A2.
 XX PD 25-AUG-2005.
 XX PF 09-FEB-2005; 2005WO-US004865.
 XX PR 09-FEB-2004; 2004US-0542939P.
 XX PR 03-FEB-2004; 2004US-0542940P.
 XX PR 09-FEB-2004; 2004US-0542963P.
 XX PR 09-FEB-2004; 2004US-0543119P.
 XX PR 18-JUN-2004; 2004US-0580791P.
 XX PR 18-JUN-2004; 2004US-0580939P.
 XX PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX PI Croce CM, Liu C, Calin GA;
 XX DR WPI; 2005-571622/58.
 XX PT Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer, tumors, or myelodysplastic syndrome, comprises evaluating a miR gene in the test sample.

XX PS Example 10; SEQ ID NO 325; 170pp; English.

CC The invention describes diagnosing whether a subject has, or is at risk
 CC for developing, a cancer linked to a cancer-associated chromosomal
 CC feature, comprises evaluating the status in the subject of at least one
 CC miRNA (miR) gene located in close proximity to the cancer-associated
 CC chromosomal feature. Also described are a pharmaceutical composition
 CC comprising an isolated miR gene product or a nucleic acid encoding an
 CC isolated miR gene product from an miR gene located in close proximity to
 CC a cancer-associated chromosomal feature and is not miR15 or miR16 and a
 CC pharmaceutical carrier; and a method of treating cancer associated with a
 CC cancer-associated chromosomal feature in a subject. The miR, composition,
 CC and method are useful for diagnosing and treating a cancer-associated
 CC chromosomal feature, where the cancer is bladder cancer, esophageal
 CC cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer,
 CC ovarian cancer, breast cancer, lymphoma, Ewing's sarcoma, hematopoietic
 CC tumors, solid tumors, gastric cancer, colorectal cancer, brain cancer,
 CC epithelial cancer, nasopharyngeal cancer, uterine cancer, hepatic cancer,
 CC head-and-neck cancer, renal cancer, male germ cell tumors, malignant
 CC mesothelioma, myelodysplastic syndrome, pancreatic or biliary cancer,
 CC prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilms' tumor,
 CC neuroblastoma, leukemia, (acute lymphocytic leukemia, acute myeloid
 CC leukemia, chronic lymphocytic leukemia), glioblastoma multiforme,
 CC medulloblastoma, lymphoplasmacytoid lymphoma, rhabdomyosarcoma, B-cell
 CC chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia
 CC associated with an unmutated IgH gene, ZAP-70 expression, CD38
 CC expression, a deletion at chromosome 11q23, a loss or mutation of TP53 or
 CC their combination. This sequence represents a human microRNA (miRNA) gene
 CC probe used in the creation of an oligonucleotide microchip for miRNA
 CC profiling.

XX

QY 1 CCUUGGAGUAAUGGUAGCAGCACAUAAUGGUUGGUU 40
 Db 1 CCTTGAGCTTAACTAGCAGCACTAATGTTGTTGGAATT 40

RESULT 14

SQ Sequence 40 BP; 11 A; 5 C; 11 G; 13 T; 0 U; 0 Other;
 AEB92913 48.2%; Score 40; DB 14; Length 40;
 ID Best Local Similarity 67.5%; Pred. No. 0.00011;
 AC Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

(UYJE-) UNTV JEFFERSON THOMAS.
croce CM, Calin GA;
WPI; 2004-400825/37.

Claim 64: SEQ ID NO 1; 73pp; English.

This invention relates to a novel method of treating an miR15 or miR16 mediated cancer in a subject which comprises administering to the subject an amount of an isolated miR15 or miR16 gene product such that proliferation of miR15 or miR16 mediated cancer cells is inhibited. The miR15 and miR16 micro RNA genes are localised to 13q14 in humans, a region that is deleted in a significant portion of subjects suffering from chronic lymphocytic leukaemia or prostate cancer. The products of the miR15 and miR16 genes have also been found to inhibit the neoplastic or tumourigenic growth of chronic lymphocytic leukaemia or prostate cancer cells. The invention may be useful for the production of compounds with a cytotoxic activity. In addition the invention may also be useful for gene therapy using the miR15 or miR16 gene product. The methods and compositions are useful in diagnosing and treating miR15 or miR16 mediated cancer, i.e. chronic lymphocytic leukaemia or prostate cancer. The present sequence is that of the human miR15 precursor RNA sequence which is used in the method of the invention.

SQ Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;

Query Match Similarity Score DB Length

Matches	38;	Conservative	14;	Mismatches	31;	Indels	0;	gaps	0;
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1 CCUUGGAGAUAAAGUAGGAGCAAUAAUGGUUUGUGGAUAAAAGGAGGAGGCLAUU 60

83 CCGGAAATTGAGGAGACAAATAGGGCGACCCCTTCAAAACCAACCAAA 24

61 UGUGGUGGCCUCAAAAUACAGG 83

23 IGGIGIGIACIIAACIICLAMGG 1

Search completed: November 1, 2006. 23.24.59

JOBLIST : 399.61 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.9
OM nucleic - nucleic search, using bw model	
Run on: November 1, 2006, 20:21:19 ; Search time 3848.83 Seconds	BZ117274 CH230-11
(without alignments)	DA287889 DA287889
1205.901 Million cell updates/sec	CT1385120 Sub scrof
Title: US-10-706-798-1	CC925288 t083bilba
Perfect score: 83	CB142086 tigr-gsaa
Sequence: 1 ccuugaggaaaguagc.....gcugccucaaaaaacaagg 83	CW371850 f8bb01f0
Scoring table: IDENTITY_NUC	CX829205 JGT CAAK6
Gapop 10.0 , Gapext 1.0	CL039913 CH216-8BM
Searched: 48236798 seqs, 27959665780 residues	CO159141 FLD1-11_E
Total number of hits satisfying chosen parameters: 96473596	BZ148619 CH23-395
Minimum DB seq length: 0	AO693353 HS 5458_A
Maximum DB seq length: 200000000	CL992915 ZMMHBF00
Post-processing: Minimum Match 0%	DT1626902 EST115997
Maximum Match 100%	CZ792260 OC_Ba015
Listing first 45 summaries	CK058325 5837_rsic
Database : EST:*	AU173105 AU173105
1: gb_est1:*	CK048847 4788_rsic
2: gb_est3:*	CK035528 3521_rsic
3: gb_est4:*	CK083202 81007_rsic
4: gb_est5:*	AL088851 Arabidops
5: gb_est6:*	CX632947 GB0003N23
6: gb_htcc:*	
7: gb_est2:*	
8: gb_est7:*	
9: gb_est8:*	
10: gb_est9:*	
11: gb_gsa1:*	
12: gb_gsa2:*	
13: gb_gsa3:*	
14: gb_gsa4:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No.	Score
	Match Length
	DB ID
	Description
SUMMARIES	
ALIGMENTS	
RESULT 1	
ACCESSION	AQ672199
DEFINITION	HS_2151_B1_B12_MR_CIT_Approved_Human_Genomic_Sperm_Library_D_Homo_sapiens_genomic_clone_Plate=2151_Col=23_Row=D, genomic survey sequence.
VERSION	AQ672199
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Homo.
AUTHORS	Mahtairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
JOURNAL	1 (bases 1 to 486)
PUBLMED	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
COMMENT	Contact: Mahtairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3818 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.hgsc.washington.edu Plate: 2151 Row: D column: 23 Seq primer: M13 Reverse Class: BAC ends High quality sequence stop: 486. Location/Qualifiers
FEATURES	1. -486 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="P1:plate=2151 Col=23 Row=D" /sex="male"
C 13	29.8
C 14	35.2
C 15	34.9
C 16	34.9
C 17	28.8
C 18	28.8
C 19	34.7
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C 21	34.5
C 22	34.5
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C 24	34.2
C 25	34.2
C 26	34.2
C 27	34.2
C 28	34.0
C 29	34.0
C 30	34.0
C 31	34.0
C 32	34.0
C 33	34.0
C 34	34.0
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C 36	34.0
C 37	34.0
C 38	34.0
C 39	33.7
C 40	33.7
C 41	33.7
C 42	33.7
C 43	33.7
C 44	33.7
C 45	33.7
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/clone lib="CIT Approved Human Genomic Sperm library D"
 /note="Organ: sperm; Vector: pBelobAC1; BAC Clones in
 E-Coli DH10B"

ORIGIN

Query Match 93.0%; Score 77.2; DB 11; Length 486;
 Best Local Similarity 68.7%; Pred. No. 3.1e-15;
 Matches 57; Conservative 22; Mismatches 4; Indels 0; Gaps 0;

ORIGIN

Query Match 86.5%; Score 71.8; DB 11; Length 638;
 Best Local Similarity 72.0%; Pred. No. 2.2e-13;
 Matches 54; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

ORIGIN

QY 1 CCUGGAGAUAGUAGCAGCAUAUAGGTTGGAGAAGGCAACCAAUU 60
 Db 440 CGTTGAGTAAAGTACGAGCACTATGTTGTTGAAAGGTCACCCAT 381

ORIGIN

QY 61 UGGUGGUCUCAAAAUACAGG 83
 Db 380 TGTGCTGCTCAAGAATACAGG 358

ORIGIN

RESULT 2
 AZ938498/c
 LOCUS AZ938498 638 bp DNA linear GSS 26-APR-2001
 DEFINITION 2M0197A08F Mouse 10kb plasmid TUGC2M library Mus musculus genomic
 ACCESSION AZ938498
 KEYWORDS GSS
 ORGANISM Mus musculus (house mouse)

ORIGIN

REFERENCE 1 CCUGGAGAUAGUAGCAGCAUAUAGGTTGGAGAAGGCAACCAAUU 60
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, M., Longacre, S., Mahmoud, M., Meenem, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederauer, A., and Wright, D., Weiss, R.

ORIGIN

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dbunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0197 row: A column: 08
 Seq primer: CGTTGTAACAGACGCCAGT
 Class: Plasmid ends
 High quality sequence stop: 638.

ORIGIN

FEATURES source
 1. .638 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:0090"
 /clone="TUGC2M0197A08"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid TUGC2M library"
 /note="Vector: MNP42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://wwwjax.org/resources/documents/dnare/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative
 of pM42 (gi|372114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptored mouse DNA was annealed to
 adaptored vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 86.5%; Score 71.8; DB 11; Length 638;
 Best Local Similarity 72.0%; Pred. No. 2.2e-13;
 Matches 54; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

ORIGIN

QY 1 CCUGGAGAUAGUAGCAGCAUAUAGGTTGGAGAAGGCAACCAAUU 60
 Db 201 CCTGGAGTAACTAGCAGCACATAATGGTTGATGATGAAAGGTGAGGCCATAC 142

ORIGIN

QY 61 UGGUGGUCUCAAAAUACAGG 75
 Db 141 TGTCGTCGCTCAAA 127

ORIGIN

RESULT 3
 DR22A19S
 LOCUS DR22A19S 330 bp DNA linear GSS 27-NOV-2002
 DEFINITION Danio rerio genomic clone DK2Y-22A19, genomic survey sequence.
 ACCESSION AL793377
 VERSION AL793377.1
 KEYWORDS GSS
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio

ORIGIN

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cyprinopterygii; Cyprinidae; Danio.
 1 (bases 1 to 330)

ORIGIN

REFERENCE 1 (bases 1 to 330)
 AUTHORS Humphray,S.J., Huckle,E. and Hunt,S.E.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
 humquery@sanger.ac.uk Unpublished

ORIGIN

COMMENT This sequence was generated from the SP6 end of BAC 22A19. 22A19 is
 part of the Daniokey BAC Library created by R. Plasterk and N.V.
 Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
 Location/Qualifiers 1..330

ORIGIN

FEATURES source
 1. .330 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DK2Y-22A19"
 /tissue="testis"
 /note="vector pIndigoBAC-536"

ORIGIN

Query Match 44.3%; Score 36.8; DB 14; Length 330;
 Best Local Similarity 52.4%; Pred. No. 0.17; Mismatches 44; Conservative 17; Indels 1; Gaps 1;

ORIGIN

QY 1 CCUGGAGAUAGUAGCAGCAUAUAGGTTGGAGAAGGCAACCAAUU 59
 Db 149 CCTCTCGGACTGTAGCAGCACATAATGGTTGAGTTATAACGGGGTCCAGCGCTA 208

ORIGIN

QY 60 UGGUGGUCUCAAAAUACAGG 83
 Db 209 CTGGCTGGCAACAGCAGG 232

ORIGIN

RESULT 4
 CNS032XX
 LOCUS CNS032XX 893 bp DNA linear GSS 01-SEP-2000
 DEFINITION 207L24 of library G from Tetradon nigroviridis, genomic survey

ORIGIN

Query Match 37.3%; Score 31; DB 10; Length 348;
 Best Local Similarity 47.1%; Pred. No. 16; Mismatches 40; Conservative 18; Mismatches 25; Indels 2; Gaps 1;
 Matches 40; Conservati 18; Mismatches 25; Indels 2; Gaps 1;

Qy 1 CCTUGAGGUAGGUAGGAGCAUAGGUTG- UGGATUTGAAAGGUGGAGGCCU 53
 Db 242 CCTTAAAGTACTGTGACGAGCATGATGTTGCACTATAGTAAAGATGGAAACAT 183

Qy 59 AUGUCGUGCCUCAAAUACAGG 83
 Db 182 TATTCGCTGCTTGTAGTTAAGG 158

RESULT 7

LOCUS AZ830728 690 bp DNA linear GSS 20-FBB-2001
 DEFINITION 2m0110F10F Mouse 10kb plasmid UGGCIM library Mus musculus genomic
 ACCESSION A2830728
 VERSION A2830728.1 GI:13000636
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarhontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 690)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenem, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederauer, A., and Wright, D.; Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid insert^S

COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0110 row: F column: 10
 Seq primer: CGTTGAAACGACGCCGCACT
 Class: plasmid ends

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to

adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 36.9%; Score 30.6; DB 11; Length 690;
 Best Local Similarity 46.8%; Pred. No. 25; Mismatches 36; Conservative 12; Mismatches 29; Indels 0; Gaps 0;
 Matches 36; Conservati 12; Mismatches 29; Indels 0; Gaps 0;

Qy 7 AGUAGAGGGAGCACAUAGGUUUGGAGAUUUGAAAGGAGCCAUAGUGUCU 66
 Db 213 AGATATGGCAGCTCATACTCTCCCTTATCTGSCAAAGCTCCGTCATTTGCTGTC 272

Qy 67 GCUCAAAUACAGG 83
 Db 273 ACTCAGAAAGAGAAAG 289

RESULT 8

LOCUS CV259755/c 409 bp mRNA linear EST 22-SEP-2004
 DEFINITION WS02012.B21_D02_PTAN-IB-N-A-11_Populus trichocarpa x Populus nigra
 CDS WS02012_B21_D02_3', mRNA sequence.

ACCESSION CV259755
 VERSION CV259755.1 GI:52512730
 KEYWORDS EST.
 SOURCE BST.

ORGANISM Populus trichocarpa x Populus nigra

REFERENCE Bukaryotida; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Malpighiales; Salicaceae; Salicace; Populus.
 1 (bases 1 to 409)

AUTHORS Ralph, S., Cooper, D., Kolesova, N., Oddy, C., Butterfield, Y.,
 Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
 Babakoff, R., Brown, John, M., Chand, S., Featherstone, R., Mason, A.,
 Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K., and
 Bohmann, J.

TITLE The poplar transcriptome: Analysis of expressed sequence tags from
 multiple cDNA libraries
 Unpublished (2004)

JOURNAL Contact: Joerg Bohmann
 COMMENT Genome BC forest genomics program
 University of British Columbia
 Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
 Vancouver, British Columbia, Canada, V6T 1Z3
 Tel: 1-604-822-0282
 Fax: 1-604-822-2114
 Email: bohmann@mbl.ubc.ca
 Plate: WS02012 row: D column: 02
 High quality sequence stop: 409
 POLYA=Yes

FEATURES

source

1. -690
 /location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGC2M0110F10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse plasmid UGGCIM library"
 /note="Vector: Pwpd2nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWP42 (gi|473214|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 36.9%; Score 30.6; DB 11; Length 690;
 Best Local Similarity 46.8%; Pred. No. 25; Mismatches 36; Conservative 12; Mismatches 29; Indels 0; Gaps 0;
 Matches 36; Conservati 12; Mismatches 29; Indels 0; Gaps 0;

Qy 7 AGUAGAGGGAGCACAUAGGUUUGGAGAUUUGAAAGGAGCCAUAGUGUCU 66
 Db 213 AGATATGGCAGCTCATACTCTCCCTTATCTGSCAAAGCTCCGTCATTTGCTGTC 272

Qy 67 GCUCAAAUACAGG 83
 Db 273 ACTCAGAAAGAGAAAG 289

RESULT 8

LOCUS CV259755/c 409 bp mRNA linear EST 22-SEP-2004
 DEFINITION WS02012.B21_D02_PTAN-IB-N-A-11_Populus trichocarpa x Populus nigra
 CDS WS02012_B21_D02_3', mRNA sequence.

ACCESSION CV259755
 VERSION CV259755.1 GI:52512730
 KEYWORDS EST.
 SOURCE BST.

ORGANISM Populus trichocarpa x Populus nigra

REFERENCE Bukaryotida; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Malpighiales; Salicaceae; Salicace; Populus.
 1 (bases 1 to 409)

AUTHORS Ralph, S., Cooper, D., Kolesova, N., Oddy, C., Butterfield, Y.,
 Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
 Babakoff, R., Brown, John, M., Chand, S., Featherstone, R., Mason, A.,
 Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K., and
 Bohmann, J.

TITLE The poplar transcriptome: Analysis of expressed sequence tags from
 multiple cDNA libraries
 Unpublished (2004)

JOURNAL Contact: Joerg Bohmann
 COMMENT Genome BC forest genomics program
 University of British Columbia
 Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
 Vancouver, British Columbia, Canada, V6T 1Z3
 Tel: 1-604-822-0282
 Fax: 1-604-822-2114
 Email: bohmann@mbl.ubc.ca
 Plate: WS02012 row: D column: 02
 High quality sequence stop: 409
 POLYA=Yes

FEATURES

source

1. -409
 /location/Qualifiers
 /organism="Populus trichocarpa x Populus nigra"
 /mol_type="mRNA"
 /cultivar="Nxm6"
 /db_xref="taxon:291756"
 /clone="WS02012_D02"
 /sex="Male"
 /lab_host="E. coli DH10B T1 phage resistant cells"
 /clone_lib="PTAN-IB-N-A-11"
 /note="Vector: pBlueScript II SK (+) XR; Site 1: EcoRI (5'
 end of cDNA); Site 2: XbaI (3' end of cDNA); Saplling trees
 two metres in height and grown under greenhouse conditions
 were exposed to continuous feeding by *Cryptotryphon*
 lapathi (poplar and willow borer) adults caged on the
 sapling using mesh bags. Bark (with phloem and cambium
 attached) from within the caged region was harvested 2
 hours, 6 hours and 48 hours after the onset of treatment.
 mRNA was isolated from each tissue source independently.

and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA library construction kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10 cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

ORIGIN

Query Match 36.6%; Score 30.4; DB 8; Length 409; Best Local Similarity 42.5%; Pred. No. 27; Mismatches 34; Conservative 15; Mismatches 31; Indels 0; Gaps 0; Matches 34;

QY 2 CUGGGAGAUAGGAGCAGCACAUAAUGGUUGGGAUUAGGAGCAGGCCAUAU 61
LOCUS AZ955179 2M0221K10F Mouse 10kb plasmid UGGC2M0221K10 clone UGGC2M0221K10 F, genomic survey sequence.
DEFINITION AZ955179
VERSION AZ955179.1
KEYWORDS GSS
ORGANISM Mus musculus (house mouse)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteraria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 669)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Dugal, B., Hamil, C., Islan, H., Longacre, S., Mahmoud, M., Meenin, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss

COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Err: 0.00
Plate: 0221 Row: K Column: 10
Seq primer: CGTGTAAACGAGGCCAGT
Class: plasmid ends
High quality sequence stop: 669.
Location/Qualifiers
FEATURES
source
1. .669
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGC2M0221K10"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGC2M library"
/note="vector: PWD42v; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnarefs/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pM42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 36.6%; Score 30.4; DB 11; Length 669; Best Local Similarity 43.8%; Pred. No. 29; Mismatches 21; Indels 0; Gaps 0; Matches 28; Conservative 15; Mismatches 21; Indels 0; Gaps 0; Matches 24;

QY 11 AGUAGGAGCACAUAAUGGUUGGGAUUAGGAGCAGGCCAUAU 70
LOCUS CK791915
DEFINITION AGENCOURT 18660624 NIH MGC_230 Mus musculus cDNA clone IMAGE:308464415, mRNA sequence.
VERSION CK791915
KEYWORDS EST
ORGANISM Mus musculus (house mouse)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteraria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 826)
JOURNAL NIH-MGC <http://mgc.nci.nih.gov/>
COMMENT Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10407 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Shiroko Kimura, Atsushi Yamada, (NCI, CCR)
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: NDAM149 Row: i Column: 10
High quality sequence stop: 643.
Location/Qualifiers
FEATURES
source
1. .826
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE_30846441"
/tissue_type="pooled thyroids from 5 mice"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 230"
/note="Organ: thyroid; vector: pExpress-1; Site_1: NotI; Site_2: NotI; RNA obtained from 5 normal wild-type mice

thyroid. cDNA was primed using oligo-dT primer: 5'-pGACTAGTCTTAATGCCAGCCGCC(TT)25-3', and cloned into the EcoRV/MotI sites of pZPExpress-1. Size-selection 1.4 kb resulted in an average insert size of 1.2 kb. Normalized version of this library is NIH MGC 18gibary constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 36.6%; Score 30; DB 5; Length 826; Best Local Similarity 47.2%; Pred. No. 30; Matches 34; Conservative 12; Mismatches 26; Indels 0; Gaps 0; QY 7 AGUUAAGUGGAGCACAUAAUGGUUUGGAAUJUGAAGGCAUUGUACU 66 Db 570 AATATATTAACATGATGGAAGGACTTGAAAGGTGAGGCTTAATCTTGAT 629 QY 67 GGCUCAAAAA 78 Db 630 CCTGCATAATA 641

RESULT 11

CT734321/c Locus CT734321 657 bp DNA linear GSS 30-SEP-2003 DEFINITION genomic survey sequence.

ACCESSION

CE734321.1

VERSION

GSS

KEYWORDS

SOURCE Canis familiaris (dog)

ORGANISM

Canis familiaris

Canis

Source

1. -752
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /sex="MALE"
 /tissue_type="lateral wall of lateral ventricle"
 /cell_type="Early passage neurosphere"
 /dev_stage="Adult"
 /clone_lib="Mouse Neurosphere Normalized cDNA library"
 /note="Organ: Adult brain; Vector: pCMVSPORT6.0; A cDNA library was constructed in pCMVSPORT6.0 from RNA isolated from neurospheres of adult male and female mice. Custom normalized cDNA library by Invitrogen/ResGen"

ORIGIN

Query Match 35.9%; Score 29.8; DB 8; Length 752;
 Best Local Similarity 43.8%; Pred. No. 47; Mismatches 33; Indels 0; Gaps 0;
 Matches 32; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

Qy 11 AAGUAGCACACAUAAUGGUUUGUGGAUTUGAAAAGGUGCACCCAUAAUGGUUGCCU 70
 Db 429 AACGTGCTACTTCGGATTACAGATTTGGGAGGGCTGCTGCTGCT 488

Qy 71 CAAAAUUCAGG 83
 Db 489 CTCAGTACAGG 501

RESULT 14

BB538951
 DEFINITION BB538951 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:347515,
 ACCESSION BE538951
 VERSION BE538951.1 GI:9767596
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 832)
 AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 TITLE Wiemann,S., Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and Wiemann,S.
 JOURNAL Unpublished (2001)
 COMMENT Contact: MPS

MMPS
 Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence available.
 This clone (DKFZP686M1020) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

REFERENCE 1 (bases 1 to 832)
 AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straubberg, Ph.D.
 Email: cgs@biomedmail.nih.gov

Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINt. at:
 http://image.lnl.gov
 Plate: LILAB421 row: d column: 12
 High quality sequence start: 4
 High quality sequence stop: 563.
 FEATURES source

ORIGIN

Query Match 34.9%; Score 29; DB 1; Length 266;
 Best Local Similarity 44.3%; Pred. No. 74; Mismatches 20; Indels 0; Gaps 0;
 Matches 27; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

Qy 20 CACAUAAUGGUUUGUGGAUTUGAAAAGGUGCACCCAUAAUGGUUGCCUAAAUAUC 79
 Db 164 CACATACATGTTAACATTTCAAATGTCAGTCATGTTGGTCAATAATACA 105

Qy 80 A 80
 Db 104 A 104

ORIGIN

Query Match 35.2%; Score 29.2; DB 7; Length 832;
 Best Local Similarity 50.0%; Pred. No. 77; Mismatches 33; Indels 0; Gaps 0;
 Matches 41; Conservative 8; Mismatches 33; Indels 0; Gaps 0;

Qy 2 CUUGGAGAUAAUGGAGCACACAUAAUGGUUGGGAUUTUGAAAAGGUGCACCCAUAU 61
 /cell_type="Early passage neurosphere"
 /dev_stage="Adult"
 /clone_lib="Mouse Neurosphere Normalized cDNA library"
 /note="Organ: Adult brain; Vector: pCMVSPORT6.0; A cDNA library was constructed in pCMVSPORT6.0 from RNA isolated from neurospheres of adult male and female mice. Custom normalized cDNA library by Invitrogen/ResGen"

RESULT 15

AL01112/c
 LOCUS AL701112
 DEFINITION DKFZP686M1020_r1 686 (synonym: hlcc3) Homo sapiens mRNA linear EST 04-SEP-2003
 ACCESSION AL701112
 VERSION AL701112.1 GI:19621645
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 REFERENCE 1 (bases 1 to 266)
 AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Mewes,H.W., Weil,B. and Wiemann,S., Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and Wiemann,S.
 TITLE Unpublished (2001)
 JOURNAL Contact: MPS

MMPS
 Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence available.
 This clone (DKFZP686M1020) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES source

ORIGIN

Query Match 34.9%; Score 29; DB 1; Length 266;
 Best Local Similarity 44.3%; Pred. No. 74; Mismatches 20; Indels 0; Gaps 0;
 Matches 27; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

Qy 20 CACAUAAUGGUUUGUGGAUTUGAAAAGGUGCACCCAUAAUGGUUGCCUAAAUAUC 79
 /cell_type="Early passage neurosphere"
 /dev_stage="Adult"
 /clone_lib="pCR2.1-TOPO"
 /note="Vector: pCR2.1-TOPO"
 /clone_lib="NIH MGC 10"
 /note="Organ: Cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dN."
 Average insert size 1.5 kb. Library prepared by Life Technologies."

ORIGIN

Search completed: November 1, 2006, 22:21:04
 Job time : 3851.83 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 20:59:58 ; Search time 143.867 Seconds

1079.486 Million cell updates/sec

Title: US-10-706-798-1

Perfect score: 83

Sequence: 1 ccuungagauaaagucagc.....gcugccucaaaauacaaag 83

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameter: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTRS_COMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/P_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result #

No. Score Query

Match Length DB ID

Description

ALIGNMENTS

RESULT 1

US-09-949-016-15172

; Sequence 15172, Application US/09949016

Patent No.: 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

NAME/KEY: misc_feature

LOCATION: (1) - (33392)

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949, 016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237, 768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231, 498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 15172

LENGTH: 33392

TYPE: DNA

ORGANISM: Human

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: (1) - (33392)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15172

Query Match 34.9%; Score 29; DB 3; Length 33392;

Best Local Similarity 37.7%; Pred. No. 1.9; Gaps 0;

Matches 29; Conservative 18; Mismatches 30; Indels 0;

Splices 0; Score 29; DB 3; Length 33392;

Query 1 ccuungagauaaagucagc.....gcugccucaaaauacaaag 83

Score 29; DB 3; Length 33392;

Sequence 29986 CCCTAACTTAATAAGTTATAATCTTGTAAATTGTGAGAGCTTGTATAA 60

Sequence 1, Appli

Sequence 1, Appli

Sequence 30046 TGTCTCCATAT 30062

Sequence 18211, A

Sequence 16861, A

Sequence 11860, A

Sequence 16463, A

Sequence 16404, A

Sequence 17398, A

GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Karla
; TITLE OF INVENTION: STARCH R1 PHOSPHORYLATION PROTEINS
; FILE REFERENCE: BB1158 US CIP
; CURRENT APPLICATION NUMBER: US/09/713,273A
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 60/081,143
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: PCT/US99/07639
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 09/679,933
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 4745
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-713-273A-19

Query Match 33.3%; Score 27.6; DB 3; Length 4745;
Best Local Similarity 45.9%; Pred. No. 3.1; Mismatches 29; Indels 0; Gaps 0;
Matches 34; Conservative 11; Mismatches 29; Indels 0; Gaps 0;

QY 3 UGGAGGUAGUGGAGCACAUAAUGGUUGGGAUUUTUGAAAGGUGGAGGCAAUUUG 62
Db 1705 TTGGTGGGAGAGCAGAAACAGAGGATTGCGAAATGCGAAAGTACAGCCAGTCT 1765

QY 63 UGGUGCCUCUAAA 76
Db 1766 TGTGCAATAAAA 1779

RESULT 3
US-09-949-016-11945
; Sequence 11945; Application US/09949016
; Patient No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11945
; LENGTH: 86439
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-11945

Query Match 33.0%; Score 27.4; DB 3; Length 86440;
Best Local Similarity 43.5%; Pred. No. 11; Mismatches 26; Indels 0; Gaps 0;
Matches 30; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 9 UAAAGUAGGAGCAGCAUAAUGGUUGGGAUUUTUGAAAGGUGGAGGCAAUUUG 68
Db 49398 TACAGCAGATGCTGAACTGTATCTGGTTCTGAACATGGCATCCATGGTTCTCA 49457

QY 69 CUCAAAAU 77
Db 49458 TCGAAATT 49466

RESULT 5
US-09-949-016-15584
; Sequence 15584; Application US/09949016
; Patient No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15584
; LENGTH: 194915
; TYPE: DNA
; ORGANISM: Human
; FEATURER
; NAME/KEY: misc_feature
; LOCATION: (1)..(194915)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-15584

Query Match 33.0%; Score 27.4; DB 3; Length 194915;
Best Local Similarity 41.6%; Pred. No. 15; Mismatches 31; Indels 0; Gaps 0;
Matches 32; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 3 UGGAGGUAGUGGAGCACAUAAUGGUUGGGAUUUTUGAAAGGUGGAGGCAAUUUG 62
Db 5285 TTAGATAAGATAAAGCATATAATAATTTGACTATTTGCGAGGAGCAACTCTTG 5344

RESULT 4

QY 63 UGCUGCCUAAAGAUAC 79
 Db 5345 AGCUGCCUAACTATCC 5361

RESULT 6
 US-09-614-221A-280
 ; Sequence 280, Application US/09614221A
 ; Patent No. 672837
 ; GENERAL INFORMATION:
 ; APPLICANT: Karunanananda, Balasuloiini
 ; APPLICANT: Yu, Jaenyuk
 ; APPLICANT: Kishore, Ganesh M.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
 ; FILE REFERENCE: 16516.075
 ; CURRENT APPLICATION NUMBER: US/09/614,221A
 ; CURRENT FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/142,981
 ; PRIOR FILING DATE: 1999-07-12
 ; NUMBER OF SEQ ID NOS: 626
 ; SEQ ID NO: 280
 ; LENGTH: 3396
 ; TYPE: DNA
 ; ORGANISM: *Saccharomyces cerevisiae*
 ; US-09-614-221A-280

Query Match 32.5%; Score 27; DB 3; Length 3396;
 Best Local Similarity 40.3%; Pred. No. 4,6; Mismatches 25; Indels 0; Gaps 0;
 Matches 27; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 13 GUAGCAGCACAUAAUGGUNGGGAUUNGAAGGUGAGGGCCAUAUUGUGUGGCCUCA 72
 Db 2173 GTCAACAAAAATGTAATTGGATTGAACTGCAGAGCTCTATGCTTCAACA 2232

QY 73 AAAAUAC 79
 Db 2233 GATGTAAC 2239

RESULT 7
 US-09-487-558B-71
 ; Sequence 71, Application US/09487558B
 ; Patent No. 6949356
 ; GENERAL INFORMATION:
 ; APPLICANT: Bushy, Robert
 ; APPLICANT: Call, Brian
 ; APPLICANT: Hecht, Peter
 ; APPLICANT: Holtzman, Doug
 ; APPLICANT: Madden, Kevin
 ; APPLICANT: Maxon, Mary
 ; APPLICANT: Milne, Todd
 ; APPLICANT: No, 6949356mar, Thea
 ; APPLICANT: Rover, John
 ; APPLICANT: Salama, Sofie
 ; APPLICANT: Sherman, Amir
 ; APPLICANT: Silva, Jeff
 ; APPLICANT: Summers, Eric
 ; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
 ; FILE REFERENCE: 109372.130
 ; CURRENT APPLICATION NUMBER: US/09487,558B
 ; CURRENT FILING DATE: 2000-01-19
 ; PRIOR APPLICATION NUMBER: US 60/487,558
 ; PRIOR FILING DATE: 1999-10-20
 ; NUMBER OF SEQ ID NOS: 446
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 71
 ; LENGTH: 3396
 ; TYPE: DNA
 ; ORGANISM: *Saccharomyces cerevisiae*
 ; US-09-487-558B-71

Query Match 32.5%; Score 27; DB 3; Length 3396;
 Best Local Similarity 40.3%; Pred. No. 4,6; Mismatches 25; Indels 0; Gaps 0;
 Matches 27; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 13 GUAGCAGCACAUAAUGGUNGGGAUUNGAAGGUGAGGGCCAUAUUGUGUGGCCUCA 72
 Db 2173 GTCAACAAAAATGTAATTGGATTGAACTGCAGAGCTCTATGCTTCAACA 2232

QY 73 AAAAUAC 79
 Db 2233 GATGTAAC 2239

RESULT 8
 US-09-949-002-814
 ; Sequence 814, Application US/09949002
 ; Patent No. 690016
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CL000790
 ; CURRENT APPLICATION NUMBER: US/09/949,002
 ; CURRENT FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/231,401
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 10823
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 814
 ; LENGTH: 13614
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(13614)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-949-002-814

Query Match 32.3%; Score 26.8; DB 3; Length 13614;
 Best Local Similarity 44.3%; Pred. No. 9,1; Mismatches 27; Indels 0; Gaps 0;
 Matches 31; Conservative 12; Mismatches 27; Indels 0; Gaps 0;

QY 2 CUGUGAGUAAAGUGAGCCACAUAAUGGUNGGGAUUNGAAGGUGAGGGCCAUAU 61
 Db 3261 CTTCGAGACTGGATTAGTAATAGATGGTTATAGAGGAGGCCCTG 3320

QY 62 GUGUGUGCC 71
 Db 3321 GTRTGCCCC 3330

RESULT 9
 US-09-297-648-3922
 ; Sequence 3922, Application US/09297648
 ; Patent No. 6964868
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Lewis T.
 ; APPLICANT: Escobedo, Jaime
 ; APPLICANT: Imin, Michael A.
 ; APPLICANT: Garcia, Pablo Dominguez
 ; APPLICANT: Sidduth-Klinger, Julie
 ; APPLICANT: Reinhard, Christopher
 ; APPLICANT: Gliese, Klaus
 ; APPLICANT: Randazzo, Filippo
 ; APPLICANT: Kennedy, Giulia C.
 ; APPLICANT: Port, David
 ; APPLICANT: Kassan, Altaf
 ; APPLICANT: Lamani, George
 ; APPLICANT: Drmanac, Radmje
 ; APPLICANT: Cirkvenjakov, Radomir
 ; APPLICANT: Dickson, Mark
 ; APPLICANT: Drmanac, Snezana

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/669,408B
 FILING DATE: 03-JUL-1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/SE94/00826
 FILING DATE: 06-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: SE 9302855-3
 FILING DATE: 06-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29 768
 REFERENCE/DOCKET NUMBER: 29 768
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1555 base pairs
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE:
 LENGTH: 1555 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 288..1526
 SEQ ID NO 3922
 LENGTH: 745
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(745)
 OTHER INFORMATION: n = A,T,C or G
 US-09-297-648-3922

Query Match 31.8%; Score 26.4; DB 4; Length 745;
 Best Local Similarity 47.5%; Pred. No. 4; Mismatches 22; Indels 0; Gaps 0;
 Matches 29; Conservative 10; MisMatch 27; Pred. No. 4; Mismatches 18; Indels 0; Gaps 0;

Qy 21 ACUAUAGGUGUAGGAAUAGUGACGCCAUAUUGUGUGCCUAAAUAUACA 80
 Db 495 ACATGTTGGTGTGACGTTGACAGTGGNCCAGCCATGTGGATGCTGAGAGAGA 594

Qy 81 A 81
 Db 555 A 555

RESULT 10
 US-08-669-408B-9/c
 Sequence 9, Application US/08669408B
 Patent No. 610055
 GENERAL INFORMATION:
 APPLICANT: GUSS, Bengt
 APPLICANT: JONSSON, Hans
 APPLICANT: LINDBERG, Martin
 APPLICANT: MUELLER, Hans-Peter
 APPLICANT: RANTAMAKI, Liisa K.
 TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/949,016
 FILING DATE: 03-JUL-1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/949,016
 FILING DATE: 03-JUL-1996
 CURRENT APPLICATION NUMBER: US/09/949,016
 FILING DATE: 03-JUL-1996
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 13209
 LENGTH: 198942
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(198942)
 OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-13209


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LOCATION: (1096846)..(1096846)
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OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g

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Query Match 31.1%; Score 25.8; DB 3; Length 1664976;
 Best Local Similarity 39.3%; Pred. No. 1.2e+02;
 Matches 24; Conservative 15; Mismatches 22; Indels 0; Gaps 0;
 Qy 22 CAUAAUGGUUGUGGAUUTUGAAGAAGGUGAGGCCAUAUTUGUGGCCUCUAAAUAUACAA 81
 Db 842845 CATAATAGTTACTGGATTCATACTTGAGCCATTGTCAGTCATAA 842904
 Qy 82 G 82
 Db 842905 G 842905

RESULT 15
 US-09-949-016-30704 Application US/09949016
 ; Sequence 30704, Application US/09949016
 ; Patent No. 6812339

; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ For Windows Version 4.0
 ; SEQ ID NO: 30704
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-30704

Query Match 30.8%; Score 25.6; DB 3; Length 601;
 Best Local Similarity 52.1%; Pred. No. 8.2;
 Matches 25; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 Qy 11 AGUAGCAGCAGCAUAAUGGUUGUGGAUUTUGAAGGUGAGGCCAU 58
 Db 203 AGAAACAGCTCATATGGGATGCTTGTAAAGATGCGCTCTT 250

Search completed: November 1, 2006, 22:24:29
 Job time : 154.867 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 22:20:01 ; Search time 1989.63 seconds

(without alignments)
512.595 Million cell updates/sec

Title: US-10-706-798-1
Perfect score: 83
Sequence: 1 ccuuggagauaaguguagc.....gcuucucucaaaauacaagg 83

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description	ALIGNMENTS
1	83	100.0	83	8	US-10-706-798-1	Sequence 1, Appli
2	83	100.0	83	10	US-10-420-955-248	Sequence 248, App
3	83	100.0	83	10	US-10-490-955-305	Sequence 305, App
4	83	100.0	83	15	US-11-100-897-72	Sequence 72, Appli
5	83	100.0	83	16	US-11-220-997-1	Sequence 1, Appli
6	83	100.0	310	10	US-10-099-125-906	Sequence 906, App
7	82	98.8	110	10	US-10-905-122-128	Sequence 128, App
8	80	96.4	110	10	US-10-905-122-165	Sequence 165, App
9	61.8	74.5	70	10	US-10-909-125-1316	Sequence 1316, App
10	33.4	40.2	83	8	US-10-706-798-1	Sequence 1, Appli
11	33.4	40.2	83	10	US-10-420-955-248	Sequence 248, App
12	33.4	40.2	83	10	US-10-490-955-305	Sequence 305, App
13	33.4	40.2	83	15	US-11-100-897-72	Sequence 72, Appli
14	33.4	40.2	83	16	US-11-220-997-1	Sequence 1, Appli
15	33.4	40.2	310	10	US-10-909-125-906	Sequence 906, App
16	32.4	39.0	110	10	US-10-905-125-128	Sequence 128, App
17	31.3	48.3	4	US-09-925-062A-615810	Sequence 615810, App	

Result No.	Score	Query	Match Length	DB ID	Description	ALIGNMENTS
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2	83	100.0	83	10	US-10-420-955-248	Sequence 248, App
3	83	100.0	83	10	US-10-490-955-305	Sequence 305, App
4	83	100.0	83	15	US-11-100-897-72	Sequence 72, Appli
5	83	100.0	83	16	US-11-220-997-1	Sequence 1, Appli
6	83	100.0	310	10	US-10-099-125-906	Sequence 906, App
7	82	98.8	110	10	US-10-905-122-128	Sequence 128, App
8	80	96.4	110	10	US-10-905-122-165	Sequence 165, App
9	61.8	74.5	70	10	US-10-909-125-1316	Sequence 1316, App
10	33.4	40.2	83	8	US-10-706-798-1	Sequence 1, Appli
11	33.4	40.2	83	10	US-10-420-955-248	Sequence 248, App
12	33.4	40.2	83	10	US-10-490-955-305	Sequence 305, App
13	33.4	40.2	83	15	US-11-100-897-72	Sequence 72, Appli
14	33.4	40.2	83	16	US-11-220-997-1	Sequence 1, Appli
15	33.4	40.2	310	10	US-10-909-125-906	Sequence 906, App
16	32.4	39.0	110	10	US-10-905-125-128	Sequence 128, App
17	31.3	48.3	4	US-09-925-062A-615810	Sequence 615810, App	

Result No.	Score	Query	Match Length	DB ID	Description	ALIGNMENTS
1	83	100.0	83	8	US-10-706-798-1	Sequence 1, Appli
2	83	100.0	83	10	US-10-420-955-248	Sequence 248, App
3	83	100.0	83	10	US-10-490-955-305	Sequence 305, App
4	83	100.0	83	15	US-11-100-897-72	Sequence 72, Appli
5	83	100.0	83	16	US-11-220-997-1	Sequence 1, Appli
6	83	100.0	310	10	US-10-099-125-906	Sequence 906, App
7	82	98.8	110	10	US-10-905-122-128	Sequence 128, App
8	80	96.4	110	10	US-10-905-122-165	Sequence 165, App
9	61.8	74.5	70	10	US-10-909-125-1316	Sequence 1316, App
10	33.4	40.2	83	8	US-10-706-798-1	Sequence 1, Appli
11	33.4	40.2	83	10	US-10-420-955-248	Sequence 248, App
12	33.4	40.2	83	10	US-10-490-955-305	Sequence 305, App
13	33.4	40.2	83	15	US-11-100-897-72	Sequence 72, Appli
14	33.4	40.2	83	16	US-11-220-997-1	Sequence 1, Appli
15	33.4	40.2	310	10	US-10-909-125-906	Sequence 906, App
16	32.4	39.0	110	10	US-10-905-125-128	Sequence 128, App
17	31.3	48.3	4	US-09-925-062A-615810	Sequence 615810, App	

Publication No. US20050059005A1
 GENERAL INFORMATION:
 APPLICANT: Tuschi, Thomas
 APPLICANT: Lages-Quintana, Mariana
 APPLICANT: Lendeckel, Winfried
 APPLICANT: Meyer, Jutta
 APPLICANT: Rauhut, Reinhard
 TITLE OF INVENTION: MicroRNA Molecules
 FILE REFERENCE: 2923-613
 CURRENT APPLICATION NUMBER: US/10/490, 955
 CURRENT FILING DATE: 2004-03-29
 PRIORITY APPLICATION NUMBER: PCT/EP02/10881
 PRIORITY FILING DATE: 2002-03-27
 PRIORITY APPLICATION NUMBER: EP 02 016 772.2
 PRIORITY FILING DATE: 2002-07-26
 PRIORITY APPLICATION NUMBER: EP 02 006 712.0
 PRIORITY FILING DATE: 2002-03-22
 PRIORITY APPLICATION NUMBER: EP 01 123 453.1
 PRIORITY FILING DATE: 2001-09-28
 NUMBER OF SEQ ID NOS: 562
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 248
 LENGTH: 83
 TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-10-490-955-248

Query Match 100.0%; Score 83; DB 10; Length 83;
 Best Local Similarity 100.0%; Pred. No. 3.3e-19;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTUGGAGUAAGUAGCAGCAGCACAUAAUTGGTGGGATGGAAAGGGGAGGCCAUU 60
 Db 61 UGUGCUGCCUCAAAAUACAGG 83
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 Db 61 UGUGCUGCCUCAAAAUACAGG 83

RESULT 3
 Query Match 100.0%; Score 83; DB 10; Length 83;
 Best Local Similarity 100.0%; Pred. No. 3.3e-19;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTUGGAGUAAGUAGCAGCAGCACAUAAUTGGTGGGATGGAAAGGGGAGGCCAUU 60
 Db 61 UGUGCUGCCUCAAAAUACAGG 83

RESULT 3
 Sequence 305, Application US/10490955
 Publication No. US20050059005A1
 GENERAL INFORMATION:
 APPLICANT: Tuschi, Thomas
 APPLICANT: Lages-Quintana, Mariana
 APPLICANT: Lendeckel, Winfried
 APPLICANT: Meyer, Jutta
 APPLICANT: Rauhut, Reinhard
 TITLE OF INVENTION: MicroRNA Molecules
 FILE REFERENCE: 2923-613
 CURRENT APPLICATION NUMBER: US/10/490, 955
 CURRENT FILING DATE: 2004-09-23
 PRIORITY APPLICATION NUMBER: 60/619, 291
 PRIORITY FILING DATE: 2004-10-15
 PRIORITY APPLICATION NUMBER: 60/600, 961
 PRIORITY FILING DATE: 2004-08-12
 PRIORITY APPLICATION NUMBER: 60/590, 856
 PRIORITY FILING DATE: 2004-07-23
 PRIORITY APPLICATION NUMBER: 60/560, 148
 PRIORITY FILING DATE: 2004-04-07
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 72
 LENGTH: 83
 TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-11-100-897-72

Query Match 100.0%; Score 83; DB 15; Length 83;
 Best Local Similarity 100.0%; Pred. No. 3.3e-19;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTUGGAGUAAGUAGCAGCAGCACAUAAUTGGTGGGATGGAAAGGGGAGGCCAUU 60
 Db 1 CCTTUGGAGUAAGUAGCAGCAGCACAUAAUTGGTGGGATGGAAAGGGGAGGCCAUU 60
 Qy 61 UGUGCUGCCUCAAAAUACAGG 83
 Db 61 UGUGCUGCCUCAAAAUACAGG 83

RESULT 5
 US-11-230-992-1
 Sequence 1, Application US/11230992
 Publication No. US20060073505A1
 GENERAL INFORMATION:
 APPLICANT: Richard H. Griffey
 APPLICANT: Ravi Jain
 TITLE OF INVENTION: OLIGOMERIC COMPOUNDS EFFECTING
 TITLE OF INVENTION: DROSHA-MEDIATED CLEAVAGE
 FILE REFERENCE: COR0041US
 CURRENT APPLICATION NUMBER: US/11/230, 992
 CURRENT FILING DATE: 2005-09-20

RESULT 3
 Sequence 305, Application US/1100897
 Publication No. US20050272075A1
 GENERAL INFORMATION:
 APPLICANT: Jacobsen, Nana
 APPLICANT: Kongsbak, Lars
 APPLICANT: Kauppinen, Sakari
 APPLICANT: Etchwald, Soren Morgensthaler
 APPLICANT: Mouritzen, Peter
 APPLICANT: Nielsen, Peter Steen
 APPLICANT: Nordholm, Mikkel
 TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF microRNAs AND SMALL
 TITLE OF INVENTION: INTERFERING RNAs
 FILE REFERENCE: 50387/013004
 CURRENT APPLICATION NUMBER: US/11/100, 897
 CURRENT FILING DATE: 2005-04-07
 PRIORITY APPLICATION NUMBER: 60/648, 221
 PRIORITY FILING DATE: 2005-01-28
 PRIORITY APPLICATION NUMBER: 60/619, 291
 PRIORITY FILING DATE: 2004-10-15
 PRIORITY APPLICATION NUMBER: 60/600, 961
 PRIORITY FILING DATE: 2004-08-12
 PRIORITY APPLICATION NUMBER: 60/590, 856
 PRIORITY FILING DATE: 2004-07-23
 PRIORITY APPLICATION NUMBER: 60/560, 148
 PRIORITY FILING DATE: 2004-04-07
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 72
 LENGTH: 83
 TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-11-100-897-72

Query Match 100.0%; Score 83; DB 15; Length 83;
 Best Local Similarity 100.0%; Pred. No. 3.3e-19;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTUGGAGUAAGUAGCAGCAGCACAUAAUTGGTGGGATGGAAAGGGGAGGCCAUU 60
 Db 1 CCTTUGGAGUAAGUAGCAGCAGCACAUAAUTGGTGGGATGGAAAGGGGAGGCCAUU 60
 Qy 61 UGUGCUGCCUCAAAAUACAGG 83
 Db 61 UGUGCUGCCUCAAAAUACAGG 83

RESULT 3
 Sequence 305, Application US/1100897
 Publication No. US20050272075A1
 GENERAL INFORMATION:
 APPLICANT: Richard H. Griffey
 APPLICANT: Ravi Jain
 TITLE OF INVENTION: OLIGOMERIC COMPOUNDS EFFECTING
 TITLE OF INVENTION: DROSHA-MEDIATED CLEAVAGE
 FILE REFERENCE: COR0041US
 CURRENT APPLICATION NUMBER: US/11/230, 992
 CURRENT FILING DATE: 2005-09-20

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; PRIOR APPLICATION NUMBER: 60/612, 059
; PRIOR FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 83
; TYPE: RNA
; ORGANISM: H. Sapiens
; US-11-230-992-1

; Query Match 100.0%; Score 83; DB 10; Length 310;
; Best Local Similarity 73.5%; Pred. No. 5.1e-19;
; Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
; LENGTH: 310
; TYPE: DNA
; ORGANISM: H. sapiens
; US-10-909-125-906

; Sequence 906, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freir, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Marcusson, Brenda F.
; APPLICANT: Koller, Eric G.
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Vickers, Timothy
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcusson, Brenda F.
; APPLICANT: Koller, Eric
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
; FILE REFERENCE: IS1008-100 (CORE01CUS)
; CURRENT APPLICATION NUMBER: US/10/909-125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/1492, 056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516, 303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531, 596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562, 417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 110
; TYPE: RNA
; ORGANISM: H. sapiens
; US-10-909-125-128

; Query Match 98.8%; Score 82; DB 10; Length 110;
; Best Local Similarity 100.0%; Pred. No. 8.3e-19;
; Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; LENGTH: 110
; TYPE: DNA
; ORGANISM: H. sapiens
; US-10-909-125-906

; Sequence 165, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcusson, Brenda F.
; APPLICANT: Koller, Eric
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
; FILE REFERENCE: IS1008-100 (CORE01CUS)
; CURRENT APPLICATION NUMBER: US/10/909-125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/1492, 056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516, 303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531, 596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562, 417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 110
; TYPE: RNA
; ORGANISM: H. sapiens
; US-10-909-125-128

; Query Match 100.0%; Score 83; DB 10; Length 310;
; Best Local Similarity 73.5%; Pred. No. 5.1e-19;
; Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
; LENGTH: 310
; TYPE: DNA
; ORGANISM: H. sapiens
; US-10-909-125-906

; Sequence 128, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcusson, Brenda F.
; APPLICANT: Koller, Eric
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
; FILE REFERENCE: IS1008-100 (CORE01CUS)
; CURRENT APPLICATION NUMBER: US/10/909-125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/1492, 056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516, 303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531, 596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562, 417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 110
; TYPE: RNA
; ORGANISM: H. sapiens
; US-10-909-125-128

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RESULT⁹
US-10-909-125-1316
; Sequence 1316, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda P.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Koller, Erich
; APPLICANT: Swazey, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peraita, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
; TITLE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: IS150080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US110/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SEQ ID NO: 165
; LENGTH: 110
; TYPE: RNA
; ORGANISM: H. sapiens
; US-10-909-125-165

Query Match 96.4%; Score 80; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 4.3e-18; Mismatches 0; Indels 0; Gaps 0;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTUGGAGUAAGUNGCGACAGCAUAAAUGGUTGGGAUTUGAAAGGUGCAAGCCAU 60
Db 31 CCTUGGAGUAAGUNGCGACAGCAUAAAUGGUTGGGAUTUGAAAGGUGCAAGCCAU 90

QY 61 UGUGCUGGCCUCAAAUACA 80
Db 91 UGUGCUGGCCUCAAAUACA 110

RESULT⁹
US-10-706-798-1/C
; Sequence 1, Application US/10706798
; Publication No. US20040152112A1
; GENERAL INFORMATION:
; APPLICANT: Croke, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: Compositions and Methods For Cancer
; TITLE OF INVENTION: Diagnosis and Therapy
; FILE REFERENCE: 08321-0126US1
; CURRENT APPLICATION NUMBER: US 10/706,798
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,864
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/469,464
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 1
; LENGTH: 83
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-706-798-1

Query Match 40.2%; Score 33.4; DB 8; Length 83;
Best Local Similarity 45.8%; Pred. No. 0.15; Mismatches 31; Indels 0; Gaps 0;
Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

QY 1 CCTUGGAGUAAGUNGCGACAGCAUAAAUGGUTGGGAUTUGAAAGGUGCAAGCCAU 60
Db 83 CCTTGATTTGGGGCGACACATATGCCCTGACCTTCAAAATCCACAAACCA 24

QY 61 UGUGCUGGCCUCAAAUACAAGG 83
Db 23 TGTCTGACTTTCTCCAGG 1

RESULT¹¹
US-10-490-955-249/C
; Sequence 249, Application US/10490955
; Publication No. US20050059005A1
; GENERAL INFORMATION:
; APPLICANT: Tuschl, Thomas
; APPLICANT: Lagos-Quintana, Mariana
; APPLICANT: Landeteil, Winfried
; APPLICANT: Meyer, Jutta
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2922-613
; CURRENT APPLICATION NUMBER: US 10/490,955
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10881
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: EP 02 016 772.2
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: EP 02 006 712.0
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01 123 453.1
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SEQ ID NO: 1316
; LENGTH: 70
; TYPE: RNA
; ORGANISM: Mouse
; US-10-909-125-1316

Query Match 74.5%; Score 61.8; DB 10; Length 70;

RESULT 12
 US-10-490-955-305/c
 ; Sequence 305, Application US/10490955
 ; Publication No. US20050039005A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tuschl, Thomas
 ; APPLICANT: Igles-Quintana, Mariana
 ; APPLICANT: Lendeckel, Winfried
 ; APPLICANT: Meyer, Jutta
 ; APPLICANT: Raab, Reinhard
 ; TITLE OF INVENTION: MicroRNA Molecules
 ; FILE REFERENCE: 2923-613
 ; CURRENT APPLICATION NUMBER: US/10/490,955
 ; CURRENT FILING DATE: 2004-03-29
 ; PRIORITY APPLICATION NUMBER: PCT/EP02/10881
 ; PRIORITY FILING DATE: 2002-09-27
 ; PRIORITY APPLICATION NUMBER: EP 02 016 772.2
 ; PRIORITY FILING DATE: 2002-07-26
 ; PRIORITY APPLICATION NUMBER: EP 02 006 712.0
 ; PRIORITY FILING DATE: 2002-03-22
 ; PRIORITY APPLICATION NUMBER: EP 01 123 453.1
 ; PRIORITY FILING DATE: 2001-09-28
 ; NUMBER OF SEQ ID NOS: 562
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 305
 ; LENGTH: 83
 ; TYPE: RNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: D. melanogaster or H. sapiens or M. musculus or C. elegans or
 ; OTHER INFORMATION: Hela cells
 ; OTHER INFORMATION: US-10-490-955-305

Query Match 40.2%; Score 33.4; DB 10; Length 83;
 Best Local Similarity 45.8%; Pred. No. 0.15; Mismatches 31; Indels 0; Gaps 0;
 Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CCTUGGAGUAAGUAGCAGCAUCUAUAGGUUAGGAGGAGGCCAUU 60
 Db 83 CCTGTGATTTTGGAGGAGCACATATGCCGTCACCTTCAAAATCCACAAACATTA 24

Qy 61 UGUGCUGCCUCAAAAUCAAGG 83
 Db 23 TGTGCTGCTACTTACTCCAGG 1

RESULT 13
 US-11-100-897-72/c
 ; Sequence 72, Application US/11100897
 ; Publication No. US20050212075A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobsen, Nana
 ; APPLICANT: Kongsbak, Lars
 ; APPLICANT: Kauppinen, Sakari

Query Match 40.2%; Score 33.4; DB 16; Length 83;
 Best Local Similarity 45.8%; Pred. No. 0.15; Mismatches 31; Indels 0; Gaps 0;
 Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CCTUGGAGUAAGUAGCAGCAUCUAUAGGUUAGGAGGAGGCCAUU 60
 Db 83 CCTGTGATTTTGGAGGAGCACATATGCCGTCACCTTCAAAATCCACAAACATTA 24

Qy 61 UGUGCUGCCUCAAAAUCAAGG 83
 Db 23 TGTGCTGCTACTTACTCCAGG 1

RESULT 14
 US-11-230-992-1/c
 ; Sequence 1, Application US/11230992
 ; Publication No. US20060073505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Richard H. Griffey
 ; APPLICANT: Ravi Jain
 ; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS EFFECTING
 ; FILE REFERENCE: COR00041US
 ; CURRENT APPLICATION NUMBER: US/11/230,992
 ; PRIORITY FILING DATE: 2004-09-21
 ; PRIORITY FILING DATE: 2005-09-20
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 83
 ; TYPE: RNA
 ; ORGANISM: H. Sapiens
 ; OTHER INFORMATION: US-11-230-992-1

Query Match 40.2%; Score 33.4; DB 16; Length 83;
 Best Local Similarity 45.8%; Pred. No. 0.15; Mismatches 31; Indels 0; Gaps 0;
 Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CCTUGGAGUAAGUAGCAGCAUCUAUAGGUUAGGAGGAGGCCAUU 60
 Db 83 CCTGTGATTTTGGAGGAGCACATATGCCGTCACCTTCAAAATCCACAAACATTA 24

Qy 61 UGUGCUGCCUCAAAAUCAAGG 83
 Db 23 TGTGCTGCTACTTACTCCAGG 1

RESULT 15
 US-10-09-125-906/c
 ; Sequence 906, Application US/10909125
 ; Publication No. US20050261218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ebau, Christine
 ; APPLICANT: Lollio, Bridget
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Freier, Susan M.
 ; APPLICANT: Griffey, Richard H.
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: Vickers, Timothy
 ; APPLICANT: Marcussen, Eric G.
 ; APPLICANT: Koller, Erich
 ; APPLICANT: Shayze, Eric
 ; APPLICANT: Jain, Ravi
 ; APPLICANT: Peralta, Eiguren
 ; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
 ; TITLE OF INVENTION: Of Small Non-Coding RNAs
 ; FILE REFERENCE: IS100080-100 (CORE01608)
 ; CURRENT APPLICATION NUMBER: US/10909125
 ; CURRENT FILING DATE: 2004-07-30
 ; PRIORITY NUMBER: US 60/492,056
 ; PRIORITY FILING DATE: 2003-07-31
 ; PRIORITY APPLICATION NUMBER: US 60/516,303
 ; PRIORITY FILING DATE: 2003-10-31
 ; PRIORITY APPLICATION NUMBER: US 60/531,596
 ; PRIORITY FILING DATE: 2003-12-19
 ; PRIORITY APPLICATION NUMBER: US 60/562,417
 ; PRIORITY FILING DATE: 2004-04-14
 ; NUMBER OF SEQ ID NOS: 2184
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 906
 ; LENGTH: 310
 ; TYPE: DNA
 ; ORGANISM: H. sapien
 ; US-10-09-125-906

Query Match 40.2%; Score 33.4; DB 10; Length 310;
 Best Local Similarity 45.8%; Pred. No. 0.23; 31; Indels 0; Gaps 0;
 Matches 38; Conservatv 14; Mismatches 31;

Qy	1	CCUUGGAGUAGAUGGAGCAGCACAUAAUGGUUUGGAGAAAGUGGAGCCAUU	60
Db	213	CCTGTATTTTGAGCCAGCACATATGGCTGACCTTCAATCCACACATTAA	154
Qy	61	UGGUGUGCCUCAAAAUAACAGGG	83
Db	153	TGTTGCTGCTACTTTACTCCAGG	131

Search completed: November 2, 2006, 02:46:34
 Job time : 1990.63 secs

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Om nucleic - nucleic search, using sw model

Run on: November 1, 2006, 22:25:14 ; Search time 187.343 Seconds
 (without alignments)
 859.641 Million cell updates/sec

Title: US-10-706-798-1

Perfect score: 83.

Sequence: 1 ccuugaggaaaguagcgc.....gcugccucaaaauacaagg 83

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2461376 seqs, 970166171 residues

Total number of hits satisfying chosen parameters: 4922752

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_New.*

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 2: /EMC_Celerra_SIDS3/ptodata/2/pupna/US05_NEW_PUB.seq: *
 3: /EMC_Celerra_SIDS3/ptodata/2/pupna/US07_NEW_PUB.seq: *
 4: /EMC_Celerra_SIDS3/ptodata/2/pupna/US08_NEW_PUB.seq: *
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 9: /EMC_Celerra_SIDS3/ptodata/2/pupna/US11_NEW_PUB.seq: *
 10: /EMC_Celerra_SIDS3/ptodata/2/pupna/US60_NEW_PUB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	83	100.0	83	US-11-194-055-33
2	83	100.0	83	US-11-375-650-1
3	83	100.0	347503	A
4	79	95.2	108	US-11-194-055-32
5	40	48.2	40	US-11-194-055-325
6	33.4	40.2	83	US-11-194-055-326
7	33.4	40.2	83	US-11-194-055-33
8	33.4	40.2	83	US-11-375-650-1
9	33.4	40.2	347503	A
10	29.6	35.7	108	US-11-194-055-32
11	28	33.7	1313	US-10-449-902-2754
12	28	33.7	1385	US-10-449-902-2804B
13	28	33.7	5689	US-11-218-305-15422
14	27.4	33.0	333	US-11-266-748B-32989
15	27.4	33.0	333	US-11-194-055-33
16	27.2	32.8	98	US-11-194-055-33
17	27	32.3	3103	US-10-539-218-3283
18	26.8	32.3	3993	US-10-539-218-3283
19	26.8	32.3	3993	US-10-539-218-3283
20	26.4	31.8	102	US-11-218-305-17846
21	26.4	31.8	181179	US-11-266-748B-31130
22	26.2	31.6	810	US-11-434-157-9301
23	26.2	31.6	810	US-11-434-157-9301
24	26.2	31.6	810	US-11-434-193-9301
25	26.2	31.6	813	US-11-348-413-7433
26	26.2	31.6	228006	US-10-440-899-119
27	26.2	31.6	2160266	US-11-434-184-10967
28	26.2	31.6	2160266	US-11-434-184-10967
29	26.2	31.6	2160266	US-11-434-184-10967
30	26.2	31.6	2160266	US-11-434-184-10967
31	26.2	31.6	2160266	US-11-434-203-10967
32	26	31.3	1389	US-11-056-355B-1552
33	26	31.3	3033	US-11-218-305-6399
34	25.8	31.1	2085	US-11-299-286-1012
35	25.8	31.1	2085	US-11-056-355B-71883
36	25.8	31.1	88208	US-10-669-920-909
37	25.8	31.1	88445	US-10-539-728-724
38	25.8	31.1	17460	US-10-540-898-497
39	25.4	30.6	1000	US-11-266-748B-291747
40	25.4	30.6	1000	US-11-266-748B-343176
41	25.4	30.6	1000	US-11-266-748B-403264
42	25.4	30.6	1000	US-11-266-748B-47310
43	25.4	30.6	2414	US-11-217-52B-8258
44	25.4	30.6	3360	US-11-217-52B-8258
45	25.4	30.6	82374	US-11-217-52B-8258

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	83	100.0	83	US-11-194-055-33
2	83	100.0	83	US-11-375-650-1
3	83	100.0	347503	A
4	79	95.2	108	US-11-194-055-32
5	40	48.2	40	US-11-194-055-325
6	33.4	40.2	83	US-11-194-055-326
7	33.4	40.2	83	US-11-194-055-33
8	33.4	40.2	83	US-11-375-650-1
9	33.4	40.2	347503	A
10	29.6	35.7	108	US-11-194-055-32
11	28	33.7	1313	US-10-449-902-2754
12	28	33.7	1385	US-10-449-902-2804B
13	28	33.7	5689	US-11-218-305-15422
14	27.4	33.0	333	US-11-266-748B-32989
15	27.4	33.0	333	US-11-194-055-33
16	27.2	32.8	98	US-11-194-055-33
17	27	32.3	3103	US-10-539-218-3283
18	26.8	32.3	3993	US-10-539-218-3283
19	26.8	32.3	3993	US-10-539-218-3283
20	26.4	31.8	102	US-11-218-305-17846
21	26.4	31.8	181179	US-11-266-748B-31130
22	26.2	31.6	810	US-11-434-157-9301
23	26.2	31.6	810	US-11-434-157-9301
24	26.2	31.6	810	US-11-434-193-9301
25	26.2	31.6	813	US-11-348-413-7433
26	26.2	31.6	228006	US-10-440-899-119
27	26.2	31.6	2160266	US-11-434-184-10967
28	26.2	31.6	2160266	US-11-434-184-10967
29	26.2	31.6	2160266	US-11-434-184-10967
30	26.2	31.6	2160266	US-11-434-184-10967
31	26	31.3	1389	US-11-056-355B-1552
32	26	31.3	3033	US-11-218-305-6399
33	26	31.3	3033	US-11-218-305-6399
34	25.8	31.1	2085	US-11-299-286-1012
35	25.8	31.1	2085	US-11-056-355B-71883
36	25.8	31.1	88208	US-10-669-920-909
37	25.8	31.1	88445	US-10-539-728-724
38	25.8	31.1	17460	US-10-540-898-497
39	25.4	30.6	1000	US-11-266-748B-291747
40	25.4	30.6	1000	US-11-266-748B-343176
41	25.4	30.6	1000	US-11-266-748B-403264
42	25.4	30.6	1000	US-11-266-748B-47310
43	25.4	30.6	2414	US-11-217-52B-8258
44	25.4	30.6	3360	US-11-217-52B-8258
45	25.4	30.6	82374	US-11-217-52B-8258

SEQUENCES

Result No.	Score	Query Match Length	DB ID	Description
1	83	100.0	83	US-11-194-055-33
2	83	100.0	83	US-11-375-650-1
3	83	100.0	347503	A
4	79	95.2	108	US-11-194-055-32
5	40	48.2	40	US-11-194-055-325
6	33.4	40.2	83	US-11-194-055-326
7	33.4	40.2	83	US-11-194-055-33
8	33.4	40.2	83	US-11-375-650-1
9	33.4	40.2	347503	A
10	29.6	35.7	108	US-11-194-055-32
11	28	33.7	1313	US-10-449-902-2754
12	28	33.7	1385	US-10-449-902-2804B
13	28	33.7	5689	US-11-218-305-15422
14	27.4	33.0	333	US-11-266-748B-32989
15	27.4	33.0	333	US-11-194-055-33
16	27.2	32.8	98	US-11-194-055-33
17	27	32.3	3103	US-10-449-902-2804B
18	26.8	32.3	3993	US-10-539-218-3283
19	26.8	32.3	3993	US-10-539-218-3283
20	26.4	31.8	102	US-11-218-305-17846
21	26.4	31.8	181179	US-11-266-748B-31130
22	26.2	31.6	810	US-11-434-157-9301
23	26.2	31.6	810	US-11-434-157-9301
24	26.2	31.6	810	US-11-434-193-9301
25	26.2	31.6	813	US-11-348-413-7433
26	26.2	31.6	228006	US-10-440-899-119
27	26.2	31.6	2160266	US-11-434-184-10967
28	26	31.3	1389	US-11-056-355B-1552
29	26	31.3	3033	US-11-218-305-6399
30	26	31.3	3033	US-11-218-305-6399
31	26	31.3	3033	US-11-218-305-6399
32	25.8	31.1	2085	US-11-299-286-1012
33	25.8	31.1	2085	US-11-056-355B-71883
34	25.8	31.1	88208	US-10-669-920-909
35	25.8	31.1	88445	US-10-539-728-724
36	25.8	31.1	17460	US-10-540-898-497
37	25.4	30.6	1000	US-11-266-748B-291747
38	25.4	30.6	1000	US-11-266-748B-343176
39	25.4	30.6	1000	US-11-266-748B-403264
40	25.4	30.6	1000	US-11-266-748B-47310
41	25.4	30.6	2414	US-11-217-52B-8258
42	25.4	30.6	3360	US-11-217-52B-8258
43	25.4	30.6	82374	US-11-217-52B-8258

RESULT 2

; Sequence 1, Application US/11375650
; Publication No. US200601165659A1
; GENERAL INFORMATION:
; APPLICANT: Crote, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: Compositions and Methods for Cancer Diagnosis and Therapy

FILE REFERENCE: 08321-0126US1
; CURRENT APPLICATION NUMBER: US/11/375,650
; CURRENT FILING DATE: 2006-03-13
; PRIOR APPLICATION NUMBER: US/10/706,798
; PRIOR FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: 60/425,864
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/469,464
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 83
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-375-650-1

Query Match 100.0%; Score 83; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.2e-20; Mismatches 0; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTUGGAGUAAGUAGCAGCACAUAGGTTGGATGAAUUGGAAAGGGCAGGCCAUU 60
Db 1 CCTUGGAGUAAGUAGCAGCACAUAGGTTGGATGAAUUGGAAAGGGCAGGCCAUU 60

Qy 61 UGGUGUGGCCUCAAAUACAGG 83
Db 61 UGGUGUGGCCUCAAAUACAGG 83

RESULT 3

US-11-286-748A-23474/C
; Sequence 23474, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/7700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996

Query Match 100.0%; Score 83; DB 8; Length 347503;
Best Local Similarity 73.5%; Pred. No. 2.4e-19; Mismatches 0; Indels 0; Gaps 0;
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTUGGAGUAAGUAGCAGCACAUAGGTTGGATGAAUUGGAAAGGGCAGGCCAUU 60
Db 52198 CCTGGAGTTAGTAGCAGCAGCTAATGGTTGTGGATTGAAAGGTGCAGGCCAT 52139

Qy 61 UGGUGUGGCCUCAAAUACAGG 83
Db 52138 TGTCCTGCCTCAAAUACAGG 52116

RESULT 4

US-11-194-055-32

; Sequence 32, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Crote, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH miRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL FEATURES

FILE REFERENCE: 3599-1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/563
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 32
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-194-055-32

Query Match 95.2%; Score 79; DB 8; Length 108;
Best Local Similarity 72.2%; Pred. No. 3.6e-19; Mismatches 0; Indels 0; Gaps 0;
Matches 57; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTUGGAGUAAGUAGCAGCACAUAGGTTGGATGAAUUGGAAAGGGCAGGCCAUU 60
Db 30 CCTUGGAGUAAGUAGCAGCACAUAGGTTGGATGAAUUGGAAAGGGCAGGCCAUU 60

Qy 61 UGGUGUGGCCUCAAAUAC 79
Db 90 TGTCCTGCCTCAAAUAC 108

RESULT 5

US-11-194-055-325
; Sequence 325, Application US/11194055

Publication No. US20060165659A1
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo M.
 TITLE OF INVENTION: Diagnoses and Methods for Cancer
 FILE REFERENCE: 08321-0126US1
 CURRENT APPLICATION NUMBER: US/11/375, 650
 CURRENT FILING DATE: 2006-03-13
 PRIOR APPLICATION NUMBER: US/10/706, 798
 PRIOR FILING DATE: 2005-11-12
 PRIOR APPLICATION NUMBER: 60/425, 864
 PRIOR FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: 60/469, 464
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 83
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-375-650-1

RESULT 9
 Query Match 40.2%; Score 33.4; DB 9; Length 83;
 Best Local Similarity 45.8%; Pred. No. 0.013; DB 9; Length 83;
 Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CCTUGGAGUAGAUGGAGCAGACAUAGAUUUGUUGGAAAGGGCAGCCAU 60
 83 CCTCTATTTTGAGGCAGACATAATGGCCGCTTGACCTTCAATCCACATTA 24
 Db 61 UGUGUGUGCCUCAAAAUACAGG 83
 23 TGTGCTGCTACTTACTCCAGG 1

RESULT 10
 US-11-194-055-32/C
 Sequence 32, Application US/11/194/055
 Publication No. US20060105360A1
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo M.
 APPLICANT: Liu, Chang-Gong
 APPLICANT: Cinzia, Sevignani
 APPLICANT: Calin, George, A.
 TITLE OF INVENTION: Diagnoses and Treatment of Cancers with
 Title of Invention: MicroRNA Located in or Near Cancers Associated Chromosomal
 Features
 FILE REFERENCE: 389-1018-008
 CURRENT APPLICATION NUMBER: US/11/194, 055
 CURRENT FILING DATE: 2005-07-29
 PRIOR APPLICATION NUMBER: PCT/US2005/004865
 PRIOR FILING DATE: 2005-02-09
 PRIOR APPLICATION NUMBER: 60/543, 119
 PRIOR FILING DATE: 2004-02-09
 PRIOR APPLICATION NUMBER: 60/542, 929
 PRIOR FILING DATE: 2004-02-09
 PRIOR APPLICATION NUMBER: 60/542, 963
 PRIOR FILING DATE: 2004-02-09
 PRIOR APPLICATION NUMBER: 60/542, 940
 PRIOR FILING DATE: 2004-02-09
 PRIOR APPLICATION NUMBER: 60/580, 959
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 60/580, 797
 PRIOR FILING DATE: 2004-06-18
 NUMBER OF SEQ ID NOS: 663
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 32
 LENGTH: 108
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-194-055-32

RESULT 11
 US-10-449-902-2754
 Sequence 2754, Application US/10449902
 Publication No. US20060123505A1
 GENERAL INFORMATION:
 APPLICANT: National Institute of Agrobiological Sciences.
 APPLICANT: Bio-oriented Technology Research Advancement Institution.
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.
 TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

Query Match 40.2%; Score 33.4; DB 8; Length 347503;
 Best Local Similarity 45.8%; Pred. No. 0.26; Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;
 Matches 38; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

Qy 1 CCTUGGAGUAGAUGGAGCAGACAUAGAUUUGUUGGAAAGGGCAGCCAU 60
 Db 52116 CCTTGATTTGAGGCAGCAGACATATGCCCTGCACCTTCAAATCCACAAACATTA 52175
 Qy 61 UGUGUGUGCCUCAAAAUACAGG 83
 Db 52176 TGTGCTGCTACTTACTCCAGG 52198

RESULT 12
 US-11-194-055-32/C
 Sequence 32, Application US/11/194/055
 Publication No. US20060105360A1
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo M.
 APPLICANT: Liu, Chang-Gong
 APPLICANT: Cinzia, Sevignani
 APPLICANT: Calin, George, A.
 TITLE OF INVENTION: Diagnoses and Treatment of Cancers with
 Title of Invention: MicroRNA Located in or Near Cancers Associated Chromosomal
 Features
 FILE REFERENCE: 389-1018-008
 CURRENT APPLICATION NUMBER: US/11/194, 055
 CURRENT FILING DATE: 2005-07-29
 PRIOR APPLICATION NUMBER: PCT/US2005/004865
 PRIOR FILING DATE: 2005-02-09
 PRIOR APPLICATION NUMBER: 60/543, 119
 PRIOR FILING DATE: 2004-02-09
 PRIOR APPLICATION NUMBER: 60/542, 929
 PRIOR FILING DATE: 2004-02-09
 PRIOR APPLICATION NUMBER: 60/542, 963
 PRIOR FILING DATE: 2004-02-09
 PRIOR APPLICATION NUMBER: 60/542, 940
 PRIOR FILING DATE: 2004-02-09
 PRIOR APPLICATION NUMBER: 60/580, 959
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 60/580, 797
 PRIOR FILING DATE: 2004-06-18
 NUMBER OF SEQ ID NOS: 663
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 32
 LENGTH: 108
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-194-055-32

Query Match 35.7%; Score 29.6; DB 8; Length 108;
 Best Local Similarity 48.5%; Pred. No. 0.34; Matches 33; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

Qy 16 GCACACAUAGAUUUGUUGGAAAGGGCAGCCAUUUGUCUCCUCAA 75
 Db 97 GCACACAUAGAUUUGUUGGAAAGGGCAGCCAUUUGUCUCCUCAA 38
 Qy 76 AUCAAGG 83
 Db 37 CCTCAAGG 30

RESULT 13
 US-10-449-902-2754
 Sequence 2754, Application US/10449902
 Publication No. US20060123505A1
 GENERAL INFORMATION:
 APPLICANT: National Institute of Agrobiological Sciences.
 APPLICANT: Bio-oriented Technology Research Advancement Institution.
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.
 TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

RESULT 14
 US-11-266-748A-23474
 Sequence 23474, Application US/11/266/748A
 Publication No. US20060134663A1
 GENERAL INFORMATION:
 APPLICANT: Harkin, Paul
 APPLICANT: Johnston, Patrick
 APPLICANT: Mulligan, Karl
 TITLE OF INVENTION: Transcriptome Microarray Technology and
 Title of Invention: Methods of Using the Same
 CURRENT APPLICATION NUMBER: US/11/266, 748A
 FILE REFERENCE: 5815-0102 (31918-0)
 CURRENT APPLICATION NUMBER: US/11/266, 748A
 CURRENT FILING DATE: 2005-11-03
 PRIOR APPLICATION NUMBER: EP 04105479.2
 PRIOR FILING DATE: 2004-11-03
 PRIOR APPLICATION NUMBER: EP 04105482.6
 PRIOR FILING DATE: 2004-11-03
 PRIOR APPLICATION NUMBER: EP 04105483.4
 PRIOR FILING DATE: 2004-11-03
 PRIOR APPLICATION NUMBER: EP 04105507.0
 PRIOR FILING DATE: 2004-11-03
 PRIOR APPLICATION NUMBER: EP 04105485.9
 PRIOR FILING DATE: 2004-11-03
 PRIOR APPLICATION NUMBER: EP 04105484.2
 PRIOR FILING DATE: 2004-11-03
 PRIOR APPLICATION NUMBER: US 60/662, 276
 PRIOR FILING DATE: 2005-03-14
 PRIOR APPLICATION NUMBER: US 60/700, 293
 NUMBER OF SEQ ID NOS: 483996
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 23474
 LENGTH: 347503
 TYPE: DNA
 ORGANISM: Homo Sapiens
 US-11-266-748A-23474

FILE REFERENCE: MOA-A0205YI-US
 CURRENT APPLICATION NUMBER: US/10/449, 902
 CURRENT FILING DATE: 2003-05-29
 PRIORITY APPLICATION NUMBER: JP 2002-203269
 PRIORITY FILING DATE: 2002-05-30
 PRIORITY APPLICATION NUMBER: JP 2002-383970
 PRIORITY FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2754
 LENGTH: 1313
 TYPE: DNA
 ORGANISM: Oryza sativa
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: AK060554
 DATABASE ENTRY DATE: 2001-12-06
 S-10-449-902-2754

Query Match 33.7%; Score 28; DB 6; Length 1313;
 Best Local Similarity 44.7%; Pred. No. 3.2; Mismatches 30; Indels 0; Gaps 0;
 Matches 34; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

GENERAL INFORMATION:
 APPLICANT: National Institute of Agrobiological Sciences.
 APPLICANT: Bio-oriented Technology Research Advancement Institution.
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.
 TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 FILE REFERENCE: MOA-A0205YI-US
 CURRENT APPLICATION NUMBER: US/10/449, 902
 PRIORITY APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIORITY APPLICATION NUMBER: JP 2002-383870
 PRIORITY FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: PatentIn Ver. 2.1
 LENGTH: 1385
 TYPE: DNA
 ORGANISM: Oryza sativa
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: AK103490
 DATABASE ENTRY DATE: 2002-08-28
 S-10-449-902-2804B

RESULT 12
 S-10-449-902-2804B
 Sequence 2804B, Application US/10449902
 Publication No. US20060123505A1

GENERAL INFORMATION:
 APPLICANT: National Institute of Agrobiological Sciences.
 APPLICANT: Bio-oriented Technology Research Advancement Institution.
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.
 TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 FILE REFERENCE: MOA-A0205YI-US
 CURRENT APPLICATION NUMBER: US/10/449, 902
 PRIORITY APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIORITY APPLICATION NUMBER: JP 2002-383870
 PRIORITY FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: PatentIn Ver. 2.1
 LENGTH: 1385
 TYPE: DNA
 ORGANISM: Oryza sativa
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: AK103490
 DATABASE ENTRY DATE: 2002-08-28
 S-10-449-902-2804B

RESULT 13
 S-10-449-902-2804B
 Sequence 2804B, Application US/10449902
 Publication No. US20060123505A1

GENERAL INFORMATION:
 APPLICANT: National Institute of Agrobiological Sciences.
 APPLICANT: Bio-oriented Technology Research Advancement Institution.
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.
 TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 FILE REFERENCE: MOA-A0205YI-US
 CURRENT APPLICATION NUMBER: US/10/449, 902
 PRIORITY APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIORITY APPLICATION NUMBER: JP 2002-383870
 PRIORITY FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: PatentIn Ver. 2.1
 LENGTH: 1385
 TYPE: DNA
 ORGANISM: Oryza sativa
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: AK103490
 DATABASE ENTRY DATE: 2002-08-28
 S-10-449-902-2804B

RESULT 14
 US-11-266-748A-268472
 Sequence 268472, Application US/11266748A
 Publication No. US2006013463A1

GENERAL INFORMATION:
 APPLICANT: Harkin, Paul
 APPLICANT: Johnston, Patrick
 APPLICANT: Mulligan, Karl
 TITLE OF INVENTION: Transcriptome Microarray Technology and
 TITLE OF INVENTION: Methods of Using the Same
 FILE REFERENCE: 55815-0102 (319189)
 CURRENT APPLICATION NUMBER: US/11/266, 748A
 CURRENT FILING DATE: 2005-11-03
 PRIORITY APPLICATION NUMBER: EP 04105479.2
 PRIORITY FILING DATE: 2004-11-03
 PRIORITY APPLICATION NUMBER: EP 04105482.6
 PRIORITY FILING DATE: 2004-11-03
 PRIORITY APPLICATION NUMBER: EP 04105483.4
 PRIORITY FILING DATE: 2004-11-03
 PRIORITY APPLICATION NUMBER: EP 04105507.0
 PRIORITY FILING DATE: 2004-11-03
 PRIORITY APPLICATION NUMBER: EP 04105485.9
 PRIORITY FILING DATE: 2004-11-03
 PRIORITY APPLICATION NUMBER: EP 04105484.2
 PRIORITY FILING DATE: 2004-11-03
 PRIORITY APPLICATION NUMBER: US 60/662, 276
 PRIORITY FILING DATE: 2005-03-14
 PRIORITY APPLICATION NUMBER: US 60/700, 293

```

; NUMBER OF SEQ_ID NOS: 433996
; SOFTWARE: PatentIn Version 3.3
; SEQ_ID NO: 268472
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-268472

Query Match      33.0%;  Score 27.4;  DB 8;  Length 333;
Best Local Similarity 44.9%;  Pred. No. 3.2;  Matches 31;  Conservative 12;  Mismatches 26;  Indels 0;  Gaps 0;
Matches 31;  Conservative 12;  Mismatches 26;  Indels 0;  Gaps 0;

Qy      1 CCTUGGAGGAAAGAGCAGCAUAUGGUUUGUGAUUUGAAAGGUGGAGCCAUU 60
Db      33 CCTGGCACACAGCCAGCCATTATGGTATGAACTTGACCTTAGCAGCCATGT 92
Qy      61 UGUGCUGCC 69
Db      93 GGTCGGGCC 101

RESULT 15
US-11-266-748A-328989/C
; Sequence 328989, Application US/11266748A
; Publication No. US2006014663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11-266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ_ID NOS: 433996
; SOFTWARE: PatentIn version 3.3
; SEQ_ID NO 328989
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-328989

Query Match      33.0%;  Score 27.4;  DB 8;  Length 333;
Best Local Similarity 44.9%;  Pred. No. 3.2;  Matches 31;  Conservative 12;  Mismatches 26;  Indels 0;  Gaps 0;
Matches 31;  Conservative 12;  Mismatches 26;  Indels 0;  Gaps 0;

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Qy      61 UGUGCUGCC 69
Db      241 GGTCGGGCC 23

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Search completed: November 1, 2006, 22:37:03
Job time : 192.343 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Om nucleic - nucleic search, using sw model

Run on: November 1, 2006, 19:39:18 ; Search time 487.143 Seconds

(without alignments)
287.948 Million cell updates/sec

Title: US-10-706-798-3

Perfect score: 22

Sequence: 1 uagcagcacauaauuguugug 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 DEFINITION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
 AUTHORS Zamore, P.-D.
 TITLE Dual functional oligonucleotides for use in repressing mutant gene expression
 JOURNAL Patent: WO 2005078096-A 16 25-AUG-2005;
 University of Massachusetts (US)
 FEATURES Location/Qualifiers
 source 1. .22
 /organism="Homo sapiens"
 /mol_type="unassigned RNA"
 /db_xref="taxon:9606"
 /note="Synthetic sequence"

ORIGIN Query Match 100.0%; Score 22; DB 2; Length 22;
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 Matches 15; Conservatve 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUUGUG 22
 Db 1 TAGCAGCACATAATGGTTGTG 22

RESULT 3
 LOCUS CS185031
 DEFINITION Sequence 5 from Patent WO2005098029.
 ACCESSION CS185031
 VERSION CS185031.1 GI:78585003
 KEYWORDS . synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Jacobson,N.
 TITLE NOVEL METHODS FOR QUANTIFICATION OF miRNAs AND SMALL INTERFERING RNA'S
 JOURNAL Patent: WO 2005098029-A 5 20-OCT-2005;
 Exiqon A/S (DK)
 FEATURES Location/Qualifiers
 source 1. .22
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic sequence"

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 Best Local Similarity 68.2%; Pred. No. 1; Mismatches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUUGUG 22
 Db 1 TAGCAGCACATAATGGTTGTG 22

RESULT 4
 LOCUS CS185033
 DEFINITION Sequence 7 from Patent WO2005098029.
 ACCESSION CS185033
 VERSION CS185033.1 GI:78585005
 KEYWORDS . synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Jacobson,N.
 TITLE NOVEL METHODS FOR QUANTIFICATION OF miRNAs AND SMALL INTERFERING RNA'S
 JOURNAL Science 294 (5543), 853-858 (2001)
 PUBLMED 1679670
 REFERENCE 2 (bases 1 to 22)
 AUTHORS Tuschi,T.

JOURNAL RNAs
 Patent: WO 2005098029-A 7 20-OCT-2005;
 EXiqon A/S (DK)
 FEATURES Location/Qualifiers
 source 1. .22
 /organism="synthetic construct"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32630"
 /note="Synthetic sequence"

ORIGIN Query Match 100.0%; Score 22; DB 2; Length 22;
 Best Local Similarity 68.2%; Pred. No. 1; Mismatches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUUGUG 22
 Db 1 TAGCAGCACATAATGGTTGTG 22

RESULT 5
 LOCUS CS185099
 DEFINITION Sequence 73 from Patent WO2005098029.
 ACCESSION CS185099
 VERSION CS185099.1 GI:78585071
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
 AUTHORS Jacobson,N.
 TITLE NOVEL METHODS FOR QUANTIFICATION OF miRNAs AND SMALL INTERFERING RNA'S
 JOURNAL Patent: WO 2005098029-A 73 20-OCT-2005;
 Exiqon A/S (DK)
 FEATURES Location/Qualifiers
 source 1. .22
 /organism="Homo sapiens"
 /mol_type="unassigned RNA"
 /db_xref="taxon:9606"

ORIGIN Query Match 100.0%; Score 22; DB 2; Length 22;
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Qy 1 UAGCAGCACAUAAUGGUUGUG 22
 Db 1 TAGCAGCACATAATGGTTGTG 22

RESULT 6
 LOCUS HSA421733
 DEFINITION Homo sapiens microRNA miR-15.
 ACCESSION AW421733
 VERSION AW421733.1 GI:17646018
 KEYWORDS miRNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 DEFINITION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Iglesias-Quintana,M., Rahut,R., Lendeckel,W. and Tuschi,T.
 TITLE Identification of novel genes coding for small expressed RNAs
 JOURNAL Science 294 (5543), 853-858 (2001)
 PUBLMED 1679670
 REFERENCE 2 (bases 1 to 22)

AUTHORS Tuschi,T.

TITLE Direct Submission
 JOURNAL Submitted (05-Nov-2001) Dep. of Cellular Biochemistry, Max Planck Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
 37077, Germany
 COMMENT Related sequences: AC069475.
 FEATURES Location/Qualifiers
 SOURCE
 1. .22
 /organism="Homo sapiens"
 /mol_type="other RNA"
 /db_xref="taxon:9606"
 /chromosome="13"
 1. .22
 /note="transcribed as larger precursor from the mir-15 gene, predicted to form hairpin"

ORIGIN

Query Match 100.0%; Score 22; DB 5; Length 22;
 Best Local Similarity 68.2%; Pred. No. 1;
 Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UACGAGCACAUAAUGGUUGUG 22
 Db 1 TAGCAGCACATAATGGTTG 22

RESULT 7
 MMU459705
 LOCUS MMU459705
 DEFINITION Mus musculus microRNA mir-15a.
 ACCESSION AJ459705
 VERSION AJ459705.1 GI:120799023
 KEYWORDS microRNA mir-15a; miR-15a gene; miRNA.
 SOURCE Mus musculus (House mouse)
 ORGANISM Muscaidae; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorpha; Muroidea; Muridae; Murinae; Mus.
 1. .22
 Lagos-Quintana, M., Rauhut, R., Yalcin, A., Meyer, J., Lendeckel, W. and Tuschl, T.
 TITLE Identification of tissue-specific microRNAs from mouse
 JOURNAL Curr. Biol. 12 (9), 735-739 (2002)
 PUBMED 12007417
 REFERENCE 2 (bases 1 to 22)
 AUTHORS Tuschl, T.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-2002) Dep. of Cellular Biochemistry, Max Planck Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
 37077, Germany
 COMMENT Related sequence: TI72137197 (Trace Archive).
 FEATURES Location/Qualifiers
 SOURCE
 1. .22
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 1. .22
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 /note="transcribed as larger precursor, predicted to form hairpin"

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 Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 TAGCAGCACATAATGGTTG 22

RESULT 8
 CS189094
 LOCUS CS189094
 DEFINITION Sequence 325 from Patent WO2005078139.
 ACCESSION CS189094
 VERSION CS189094.1 GI:80750083
 FEATURES
 KEYWORDS . synthetic construct
 SOURCE Synthetic construct
 ORGANISM Other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Croce, C.M.
 JOURNAL Patent: WO 2005078139-A 325 25-AUG-2005;
 THOMAS JEFFERSON UNIVERSITY (US)
 LOCATION/Qualifiers
 1. .40
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide probe"

ORIGIN

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 Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUUGUG 22
 Db 14 TAGCAGCACATAATGGTTG 35

RESULT 9
 CS185098
 LOCUS CS185098
 DEFINITION Sequence 72 from Patent WO2005098029.
 ACCESSION CS185098
 VERSION CS185098.1 GI:78585070
 FEATURES
 KEYWORDS
 SOURCE Homo sapiens
 ORGANISM Human
 Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1. .83
 Jacobsen, N.
 TITLE NOVEL METHODS FOR QUANTIFICATION OF microRNAs AND SMALL INTERFERING RNA
 JOURNAL Patent: WO 2005098029-A 72 20-OCT-2005;
 EXIQON A/S (DK)
 FEATURES
 SOURCE location/Qualifiers
 1. .83
 /organism="Homo sapiens"
 /mol_type="unassigned RNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 83;
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Qy 1 UAGCAGCACAUAAUGGUUGUG 22
 Db 14 TAGCAGCACATAATGGTTG 35

RESULT 10
 CS188802
 LOCUS CS188802
 DEFINITION Sequence 33 from Patent WO2005078139.
 ACCESSION CS188802
 VERSION CS188802.1 GI:80749791
 FEATURES
 KEYWORDS
 SOURCE Homo sapiens (human)

Query Match /note="based on *Homo sapiens* mir-16-1"
 /product="microRNA mir-16-1"

ORIGIN

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 Db 403 TAGCAGCACATAATGGTTGTG 424

RESULT 14

AV866306 AY866306 Bpongo_pygmaeus microRNA mir-15a and microRNA mir-16-1 genes, complete sequence.

ACCESSION AY866306
 DEFINITION Bpongo_pygmaeus microRNA mir-15a and microRNA mir-16-1 genes, complete sequence.

VERSION AY866306.1 GI:57903108

KEYWORDS

ORGANISM Bpongo_pygmaeus (orangutan)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrini; Homidae; Pongo.

REFERENCE 1 (bases 1 to 747)

AUTHORS Berezikov, E., Guryev, V., van de Belt, J., Wienholds, E., Plasterk, R.H. and Cuppen, E.

TITLE Phylogenetic Shadowing and Computational Identification of Human microRNA Genes

JOURNAL Cell 120 (1), 21-24 (2005)

PUBLMED 1565478

REFERENCE 2 (bases 1 to 825)

AUTHORS Berezikov, E., Guryev, V., van de Belt, J., Wienholds, E., Plasterk, R.H. and Cuppen, E.

TITLE Direct Submission

JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaan 8, Utrecht 3584 CT, The Netherlands

FEATURES source

ORGANISM /organism="Saguinus labiatus"
 /mol_type="genomic DNA"
 /db_xref="Taxon:78454" 1..825

misc_RNA 448..530

/product="precursor microRNA mir-15a"
 /note="based on *Homo sapiens* mir-15a"

misc_RNA 461..482

/product="microRNA mir-15a"

misc_RNA 588..676

/product="precursor microRNA mir-16-1"
 /note="based on *Homo sapiens* mir-16-1"

misc_RNA 601..622

/product="microRNA mir-16-1"

REFERENCE 2 (bases 1 to 747)

AUTHORS Berezikov, E., Guryev, V., van de Belt, J., Wienholds, E., Plasterk, R.H. and Cuppen, E.

TITLE Direct Submission

JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalaan 8, Utrecht 3584 CT, The Netherlands

FEATURES source

ORGANISM /organism="Bpongo_pygmaeus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9600" 1..747..559

/product="precursor microRNA mir-15a"
 /note="based on *Homo sapiens* mir-15a"

misc_RNA 490..511

/product="microRNA mir-15a"

misc_RNA 617..705

/product="precursor microRNA mir-16-1"
 /note="based on *Homo sapiens* mir-16-1"

misc_RNA 630..651

/product="microRNA mir-16-1"

ORIGIN

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 Db 461 TAGCAGCACATAATGGTTGTG 482

Search completed: November 1, 2006, 20:59:42
 Job time : 492.143 Bees

RESULT 15

Query Match Best Local Similarity 68.2%; Pred. No. 1..6; Score 22; DB 5; Length 747;
 Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 UACGAGCACAUAAAUGGUGUG 22
 Db 490 TAGCAGCACATAATGGTTGTG 511

ACCESSION AY866302
 DEFINITION *Saguinus labiatus* microRNA mir-15a and microRNA mir-16-1 genes, complete sequence.

VERSION AY866302.1 GI:57903104

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Gencore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 1, 2006, 20:21:19 ; Search time 1020.17 Seconds
(without alignments)
1205.901 Million cell updates/sec

Title: US-10-706-798-3

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Post-processing: Minimum Match 0%
Maximum Match 100%

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12: gb_gst2:*

13: gb_gst3:*

gb_gst4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C	3	100.0	638	11 A2938438	LOCUS
C	4	19.4	88.2	445 4 BW837082	Danio rerio genomic clone DR22A19, genomic survey sequence.
C	5	19.4	88.2	627 2 BJ627722	DEFINITION
C	6	19.4	88.2	723 9 CX379068	ACCESSION
C	7	19.4	88.2	785 4 BW732390	VERSION
C	8	19.4	88.2	804 10 BW730170	KEYWORDS
C	9	19.4	88.2	884 3 BU909485	SOURCE
C	10	18.8	85.5	394 13 CL270436	ORGANISM
C	11	18.8	85.5	585 11 BH048477	Danio rerio (zebrafish)
C	12	18.8	85.5	830 4 CB502306	COMMENT
C	13	18.8	85.5	893 14 CN032XX	REFERENCE
C	14	18.4	83.6	948 10 DR75958	AUTHORS
C	15	18.4	83.6	932 1 AL654787	TITLE
C	16	17.8	80.9	191 1 A1633347	JOURNAL
C	17	17.8	80.9	421 11 A0892377	COMMENT
C	18	17.8	80.9	421 11 A0886977	COMMENT
C	19	17.8	80.9	422 8 CX082256	COMMENT

AL7739377 Danio rerio

A0672199 HS_2151-B

A2938438 2M01197A08

BW837082 BW837082

BJ627722 BJ627722

CX379068 JGI_X2T20

BW732390 BW732390

BW730170 BW730170

BU909485 AGENCOURT

CL270436 AGENCOURT

BH048477 RGT-24-3

CB502306 AGENCOURT

AL225438 Tetradon

DR975958 Skin-13-B

AL654787 AL654787

A1633347 A1633347

A0892377 A0892377

A0886977 HS_3122-B

CX082256 BHAAT87TR

ALIGNMENTS

20	17.8	80.9	473	8	CV473806	CV473806 220891. D	
21	17.8	80.9	599	8	CX088035	CX088035 EHADA56TR	
C	22	17.8	80.9	604	8	CX089370	CX089370 EHDX37TR
C	23	17.8	80.9	613	14	CZ135052	DB133052 Oryzias 1
C	24	17.8	80.9	617	13	CZ078834	CZ078834 OM_Bad07
C	25	17.8	80.9	631	8	CX097110	CX097110 EHAI195TR
C	26	17.8	80.9	670	14	CR061257	CR061257 Reverse 8
C	27	17.8	80.9	679	11	A2428541	A2428541 IM0212005
C	28	17.8	80.9	764	13	DU459257	DU459257 10942106
C	29	17.8	80.9	802	4	BX887642	BX887642 BX887642
C	30	17.8	80.9	804	13	CW837931	CW837931 DR22A63
C	31	17.8	80.9	823	11	BH161771	BH161771 ENTRC17TR
C	32	17.8	80.9	860	11	A2678560	A2678560 ENTRMS1TR
C	33	17.8	80.9	889	11	A2684626	A2684626 ENTRK65TR
C	34	17.8	80.9	983	11	BH164645	BH164645 ENTRQV7TR
C	35	17.8	80.9	1272	2	BW869305	BW869305 603396203
C	36	17.4	79.1	260	13	CW401759	CW401759 fabb01f0
C	37	17.4	79.1	271	4	BX88587	BX88587 BX88587
C	38	17.4	79.1	364	12	CE710553	CE710553 tigr-98B-
C	39	17.4	79.1	412	4	CB617339	CB617339 ESTRF14_QY
C	40	17.4	79.1	420	1	AL119702	AL119702 DK2ZP7610
C	41	17.4	79.1	459	3	BP085372	BP085372 BP085372
C	42	17.4	79.1	500	1	AU086235	AU086235 AU086235
C	43	17.4	79.1	543	2	BG410941	BG410941 EM1_27_H0
C	44	17.4	79.1	611	11	BH059786	BH059786 RIC1-27-3
C	45	17.4	79.1	627	13	CW112106	CW112106 104_485_1

RESULT 2

REFERENCE	AQ672199	486 bp	DNA	1-linear	GSS 24-JUN-1999	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
LOCUS	AQ672199					JOURNAL	Plasmid Inserts
DEFINITION	HS_2151_B1_B12_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2151 Col=23 Row=D, genomic survey sequence.					COMMENT	Unpublished (2000)
ACCESSION	AQ672199					CONTACT	Robert B. Weiss
VERSION	AQ672199.1					UNIVERSITY	University of Utah Genome Center
KEYWORDS	GSS.					RM	308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
SOURCE	Homo sapiens (human)					TEL	801 585 5606
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchoptoclyres; Primates; Catarrini; Homidae; Homo.					FAX	801 585 7177
REFERENCE	1 (bases 1 to 486)					EMAIL	datum@genetics.utah.edu
AUTHORS	Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furiong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.					INSERT LENGTH	10000 Std Error: 0.00
COMMENT	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome					PLATE	0197
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)					ROW	A
PUBLISHED	10449764					COLUMN	08
CONTACT	Email: jwallace@u.washington.edu					SEQ PRIMER	CGTTGTAACGACGGCCAGT
High Throughput Sequencing Center	Contact: Mahairas GG, Wallace JC, Hood L					CLASS	plasmid ends
401 Queen Anne Avenue North, Seattle, WA 98109, USA	High Throughput Sequencing Center					LOCATION/QUALIFIERS	High quality sequence stop: 638.
Tel: (206) 616-3618	High quality sequence stop: 638.						
Fax: (206) 616-3887	1. .486						
Email: jwallace@u.washington.edu	/organism="Homo sapiens"						
Clones may be purchased from Research Genetics (info@resgen.com).	/mol_type="genomic DNA"						
BAC end Web Server: http://www.hgsc.washington.edu	/db_xref="taxon:606"						
Plate: 2151 row: D column: 23	/clone="Plate=2151 Col=23 Row=D"						
Seq primer: M13 Reverse	/sex="mal"						
Class: BAC end	/clone lib="CIT Approved Human Genomic Sperm Library D"						
High quality sequence stop: 486.	/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"						
FEATURES	Location/Qualifiers						
SOURCE	1. .486						
Query Match	100.0%; Score 22; DB 11; Length 486;						
Best Local Similarity	68.2%; Pred. No. 6.9;						
Matches	15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;						
QY	1 UAGCAGCACAUAAUGGUUGUG 22						
Db	427 TAGCAGCACATAATGGTTGTG 406						
RESULT 3							
AZ238498/c	AZ938498	638 bp	DNA	linear	GSS 26-APR-2001	ORIGIN	
LOCUS	AZ938498					Query Match	100.0%; Score 22; DB 11; Length 638;
DEFINITION	2M0197A08F Mouse 10kb plasmid tUGC2M library Mus musculus genomic clone UUGC2M0197A08 F, genomic survey sequence.					Best Local Similarity	68.2%; Pred. No. 7.1;
ACCESSION	AZ238498					Matches	15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
VERSION	AZ238498.1					QY	1 UAGCAGCACAUAAUGGUUGUG 22
KEYWORDS	GSS.					Db	188 TAGCAGCACATAATGGTTGTG 167
SOURCE	Mus musculus (house mouse)						
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchoptoclyres; Gires; Rodentia; Murinae; Mus.						
REFERENCE	1 (bases 1 to 638)						
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenah, E., Pedersen, T., Reilly, M., Rose, R., Strokes, R., Tingey, A., von Niederhäusern, A. and Wright, D., Weiss, R.						
RESULT 4							
BW837082	BW837082	445 bp	mRNA	linear	EST 24-DEC-2005	ORGANISM	Branchiostoma floridae (Florida lancelet)
LOCUS	BW837082					DEFINITION	Branchiostoma floridae mRNA sequence.
DEFINITION	BW837082					ACCESSION	BW837082
ACCESSION	BW837082.1					VERSION	BW837082.1
VERSION	EST.					KEYWORDS	EST.
KEYWORDS						SOURCE	Branchiostoma floridae (Florida lancelet)
SOURCE						ORGANISM	Branchiostoma floridae
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Brachiostoma.						
REFERENCE	1 (bases 1 to 445)						
AUTHORS	Yu, J., Holland, L.Z., Shin-i, T., Kohara, Y., Satou, Y. and Satoh, N.						
TITLE	Expressed genes in Branchiostoma floridae						
JOURNAL	Unpublished (2005)						

COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-816856 Fax: 81-559-816856 Email: tshini@genes.nig.ac.jp If you want to have a cDNA clone for this EST or if you have any questions, please send an e-mail to Nori Satoh (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou (yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES	<p>source</p> <p>If you want to have a cDNA clone for this EST or if you have any questions, please send an e-mail to Nori Satoh (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou (yutaka@ascidian.zool.kyoto-u.ac.jp).</p> <p>Location/Qualifiers</p> <p>1. .455 'organism="Branchiostoma floridae" 'mol_type="mRNA" 'db_xref="taxon:7739" 'clone="BfLV59i18" 'tissue_type="whole animal" 'dev_stge="larva" 'clone_lib="Amphioxus Branchiostoma floridae unpublished cDNA library, larva whole animal"</p>
ORIGIN	Query Match
	Best Local Similarity 88.2%; Score 19.4; DB 4; Length 445; Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
RESULT 5	<p>Best Local Similarity 66.7%; Pred. No. 1.4e+02; DB 4; Length 445; Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;</p> <p>LOCUS BX627722 NIBB Mochii normalized Xenopus early gastrula library DEFINITION Xenopus laevis mRNA linear EST 01-OCT-2003 ACCESSION BX627722 VERSION BX627722.1 KEYWORDS EST SOURCE ORGANISM Xenopus laevis (African clawed frog) Xenopus laevis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodidae; Xenopus; Xenopus. REFERENCE AUTHORS Kitayama,A., Terasaki,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y. TITLE Unpublished (2001) JOURNAL Contact: Tadasu Shin-i COMMENT Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-816856 Fax: 81-559-816856 Email: tshini@genes.nig.ac.jp The information of this clone is available through the following URL: http://xenopus.nibb.ac.jp.</p>
FEATURES	<p>source</p> <p>If you want to have a cDNA clone for this EST or if you have any questions, please send an e-mail to Nori Satoh (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou (yutaka@ascidian.zool.kyoto-u.ac.jp).</p> <p>Location/Qualifiers</p> <p>1. .723 'organism="Xenopus tropicalis" 'mol_type="mRNA" 'db_xref="taxon:8364" 'clone="IMAGB:7625775" 'tissue_type="whole embryo" 'dev_stge="Radpole (st. 36-41)" 'lab_host="E. coli XL1-Blue derivative, Stratagene 'ElectroPren-Blue" 'clone_lib="NIH_XGC_tcrpTad5" 'note=>vector: pCSI108; Site 1: Sall; Site 2: NotI; Radpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dT primers (Invitrogen Superscript Plasmid System for cDNA Synthesis and Cloning). Sall (5', end) -NotI (3', end) cDNA was inserted into vector pCSI108 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)</p>
ORIGIN	Query Match
	Best Local Similarity 88.2%; Score 19.4; DB 9; Length 723; Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
FEATURES	<p>source</p> <p>If you want to have a cDNA clone for this EST or if you have any questions, please send an e-mail to Nori Satoh (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou (yutaka@ascidian.zool.kyoto-u.ac.jp).</p> <p>Location/Qualifiers</p> <p>1. .723 'organism="Xenopus laevis" 'mol_type="mRNA" 'db_xref="taxon:8355" 'clone="Xk121sc06" 'tissue_type="whole embryo" 'dev_stge="stage 10.5" 'clone_lib="NIBB Mochii normalized Xenopus early gastrula library"</p>
ORIGIN	Query Match
	Best Local Similarity 88.2%; Score 19.4; DB 2; Length 627;
FEATURES	<p>source</p> <p>If you want to have a cDNA clone for this EST or if you have any questions, please send an e-mail to Nori Satoh (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou (yutaka@ascidian.zool.kyoto-u.ac.jp).</p> <p>Location/Qualifiers</p> <p>1. .723 'organism="Xenopus tropicalis" 'mol_type="mRNA" 'db_xref="taxon:8364" 'clone="IMAGB:7625775" 'tissue_type="whole embryo" 'dev_stge="stage 10.5" 'clone_lib="NIBB Mochii normalized Xenopus early gastrula library"</p>
ORIGIN	Query Match
	Best Local Similarity 88.2%; Score 19.4; DB 2; Length 627;

RESULT 7	BW723290	BW723290	785 bp	mRNA	linear	EST 22-OCT-2005		
LOCUS	BW723290	Amphioxus Branchiostoma floridae unpublished cDNA library, adult whole animal Branchiostoma floridae CDNA Clone bfdd035b06 3', mRNA sequence.						
DEFINITION	BW723290							
ACCESSION	BW723290							
VERSION	BW723290.1	GI:66309882						
KEYWORDS	BEST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	Unpublished (2005)							
COMMENT	1. (bases 1 to 785) Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp If you want to have a cDNA clone for this EST or if you have any questions, please send an e-mail to Nori Satoh (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou (yutaka@ascidian.zool.kyoto-u.ac.jp).							
JOURNAL	Tadasu Shin-i							
AUTHORS	Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
TITLE	Expressed genes in Branchiostoma floridae							
RESULT 8	BW730170	BW730170	894 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 894) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 9	BW909485	BW909485	884 bp	mRNA	linear	EST 17-OCT-2002		
DEFINITION	AGENCOURT 10481253 NICHID XGC Embl Xenopus laevis cDNA clone IMAGE 6633541 5', mRNA sequence.							
LOCUS	BW909485							
ACCESSION	BW909485							
VERSION	BW909485.1	GI:24091399						
KEYWORDS	EST							
SOURCE	Xenopus laevis (African clawed frog)							
ORGANISM	Xenopus laevis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap							
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index							
AUTHORS	Unpublished (1997)							
TITLE	Contact: Robert Strausberg, Ph.D.							
RESULT 10	BW730170	BW730170	894 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 894) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 11	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 12	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 13	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 14	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 15	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 16	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 17	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 18	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 19	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 20	BW730170	BW730170	884 bp	mRNA	linear	EST 22-OCT-2005		
DEFINITION	BW730170 Amphioxus Branchiostoma floridae unpublished cDNA clone bfad05g14 3', adult whole animal Branchiostoma floridae CDNA clone bfad05g14 3', mRNA sequence.							
LOCUS	BW730170							
ACCESSION	BW730170							
VERSION	BW730170.1	GI:66316782						
KEYWORDS	EST							
SOURCE	Branchiostoma floridae (Florida lancelet)							
ORGANISM	Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.							
FEATURES	source							
REFERENCE	1. (bases 1 to 884) Yu, J., Holland, L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.							
COMMENT	Expressed genes in Branchiostoma floridae Unpublished (2005) Contact: Tadasu Shin-i Center For Genetic Resource Information							
JOURNAL								
AUTHORS								
TITLE								
RESULT 21	BW730170	BW7						

Qy	1	UAGCAGCAGAUAUAGGUGUGU	21	CL270436/c	RESULT 10
Db	185	TAGCAGCACATCAGGTTGT	205	CL270436	Best Local Similarity 61.9%; Pred. No. 1.5e+02; Mismatches 7; Indels 0; Gaps 0;
LOCUS	CL270436	394 bp	DNA	linear	GSS 08-FEB-2005
DEFINITION	Ggal_105a_PR_B06	Ggal PR-1	Gallus gallus	genomic clone	
ACCESSION	CL270436				
VERSION	CL270436.1	GI:58747778			
KEYWORDS	GSS				
SOURCE	Gallus gallus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
REFERENCE	1 (bases 1 to 394)				
AUTHORS	Wicker, T., Robertson, J.S., Schulze, S.R., Feltus, F.A., Magrini, V., Morrison, J.A., Mardis, E.R., Wilson, R.K., Peterson, D.G., Patterson, A.H. and Marie R.				
TITLE	The repetitive landscape of the chicken genome				
JOURNAL	Genome Res. 15 (1), 126-136 (2005)				
PUBLMED	1525510				
COMMENT	Plant Genome Mapping Laboratory				
	University of Georgia, Center for Applied Genetic Technologies				
	Riverbend Research Laboratory, Room 162, 110 Riverbend Road,				
	Athens, GA 30602 USA				
	Tel: 7065330169				
	Fax: 706530160				
	Email: paterson@uga.edu				
SEQUENCE	Sequence from middle repetitive (MR) Cot fraction, Cot 10-100				
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source	Location/Qualifiers				
	1. . 394				
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ORIGIN					
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Best Local Similarity	63.6%; Pred. No. 2.8e+02; Mismatches 14; Conservative 6; Mismatches 2;				
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Db	170	TAGAACAGACAGATGGTTGT	149	CB52036	Best Local Similarity 59.1%; Pred. No. 2.9e+02; Mismatches 13; Conservative 7; Mismatches 2;
LOCUS	CB52036	830 bp	mRNA	linear	EST 02-APR-2003
DEFINITION	AGENCOURT 13324904 NICHHD XGC Tad1 Xenopus laevis cDNA clone IMAGE:6880576 3', mRNA sequence.				
ACCESSION	CB52036				
VERSION	CB52036.1	GI:29481566			
KEYWORDS	EST.				
SOURCE	Xenopus laevis (African clawed frog)				
ORGANISM	Xenopus laevis				
REFERENCE	1 (bases 1 to 830)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D.				
	Email: cgsaps-r@mail.nih.gov				
	Tissue Procurement: Drs. Donald Brown and Liqian Cai				
	CDNA Library Preparation: Clontech				
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LBNL)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LBNL at:				
REFERENCE	1 (bases 1 to 586)				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
VERSTON	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchoptoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.				
KEYWORDS					

REFERENCE 1 (bases 1 to 932)
 AUTHORS Christophides, G.K., Blass, K., Zdobnov, E.M., Carmouche, R., Benes, V., and Kafatos, F.C.
 TITLE Anopheles gambiae EST, European Molecular Biology Laboratory
 JOURNAL Unpublished (2002)
 COMMENT Contact: Christophides GK
 Email: G.Kristof.Christophides@ebi.ac.uk

European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg
Tel: +49 6221 387-440
Fax: +49 6221 387-306
Plate: christop@embl-heidelberg.de
Plate: P23 row: F Column: 06.

source 1. .932

```

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      gags sequenced from the T7 priming site that reads from
      the 5' end of cDNA. The NAPI is a directionally cloned and
      normalized, oligo-T primed cDNA library constructed from
      mixture of Anopheles gambiae developmental stages
      according to: Bonaldo, Lennon & Soares (1996):"
      Normalization and Subtraction: Two Approaches To
      Facilitate Gene Discovery, Genome Research 6, 791-806. "

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Query Match 83.6%; Score 18.4; DB 1; Length 932; Best Local Similarity 65.0%; Pred. No. 4.8e+02; Matches 13; Conservative 6; Mismatches 1; Qy 2 AGCAGCACAUAAUGGUUGU 21 Db 297 AGCAGCACATATGGTGTG 278

Search completed: November 1, 2006, 22:21:01
Job time : 1026.17 secs

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OM nucleic - nucleic search, using sw model
Run on: November 1, 2006, 19:02:55 ; Search time 105.39 Seconds
(without alignments)
1455.440 Million cell updates/sec

Title: US-10-706-798-3
Perfect score: 22
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Scoring table: IDENTITY_NTC
Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query	Match Length	DB	ID	Description
1	22	100.0	22	8	ADAO0084	RESULT 1 ADA00084
2	22	100.0	22	8	ADAO0122	ID ADA00084 standard; RNA; 22 BP.
3	22	100.0	22	12	AD017091	XX
4	22	100.0	22	12	ADP84065	AC ADA00084;
5	22	100.0	22	13	ADP83121	XX
6	22	100.0	22	14	ADP03284	DT 06-NOV-2003 (first entry)
7	22	100.0	22	14	ADP03184	XX
8	22	100.0	22	14	ADP03184	DB Human miRNA sequence miR-15 SEQ ID NO:81.
9	22	100.0	22	14	ADP03184	XX
10	22	100.0	22	14	ADP03184	XX
11	22	100.0	22	14	ADP03184	XX
12	22	100.0	22	14	ADP03184	XX
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14	22	100.0	22	14	ADP03184	XX
15	22	100.0	22	14	ADP03184	XX
16	22	100.0	22	14	ADP03184	XX
17	22	100.0	22	14	ADP03184	XX
18	22	100.0	22	14	ADP03184	XX
19	22	100.0	22	15	ADP03184	XX
20	22	100.0	22	15	ADP03184	XX
21	22	100.0	22	15	ADP03184	XX
22	22	100.0	22	15	ADP03184	XX
23	22	100.0	22	15	ADP03184	XX
24	22	100.0	22	15	ADP03184	XX
25	22	100.0	30	15	ADP00087	XX
26	22	100.0	40	14	ADP02912	XX
27	22	100.0	70	14	ADP04205	XX
28	22	100.0	83	12	AD017089	XX
29	22	100.0	83	14	ADP02620	XX
30	22	100.0	83	14	AED35990	XX
31	22	100.0	83	15	AEB26703	XX
32	22	100.0	83	15	AEB9350	XX
33	22	100.0	83	15	AEB9543	XX
34	22	100.0	108	14	AEB29619	XX
35	22	100.0	110	14	ADX3080	XX
36	22	100.0	110	14	ADX3080	XX
37	22	100.0	310	14	ADX03808	XX
38	22	100.0	4214	4	AAK72317	XX
39	21	95.5	21	8	ADA0022	XX
40	21	95.5	21	14	ADX04045	XX
41	21	95.5	21	14	ADX04624	XX
42	18.8	85.5	7808	14	ADZ45650	XX
43	18.8	85.5	7824	14	ADZ45651	XX
44	18.8	81.8	81.8	12	AD017093	XX
45	17.8	80.9	21	14	ADX85401	XX

Aed26704 Hsa miR-1

Aed26638 hsa-miR-1

Aed26636 hsa-miR-1

Aef23393 Human miR

Aef07099 Mouse miR

Aed3599 Human pri

Aef00087 DNA probe

Aeb93912 Human miR

Aeb9350 Human miR

Aeb9543 Mouse miR

Aeb29619 Human miR

Aed04045 Human mat

Adx04624 Antisense

Adx45650 Human pap

Adz45651 Human pap

Ado17093 Human miR

Adx85401 Human/ mo

CC The present invention describes an isolated nucleic acid molecule (I)

CC comprising a nucleotide sequence of *Drosophila melanogaster*, human or mouse microRNAs (miRNAs), or their precursors, a complement of it, a nucleotide sequence that hybridises under stringent conditions to them, also described: (1) a pharmaceutical composition containing the nucleic acid and, optionally, a carrier; and (2) identifying miRNA molecules or precursor molecules, comprising ligating 5'- and 3'-adapter molecules to the ends of a size-fractionated RNA population, reverse transcribing the adapter-containing RNA population and characterising the reverse transcription products. (I) has cytostatic activity, and can be used in gene therapy. The pharmaceutical composition is useful for diagnostic and therapeutic applications, and as a marker or a modulator of developmental or pathogenic processes, particularly of cancer (e.g. B-cell chronic leukaemia) or gene expression. The miRNA molecules may also be used in tissue reprogramming procedures. The present sequence represents an miRNA sequence from the present invention.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 22; DB 8; Length 22; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCGAGCACAUAAUGGUUUGUG 22
Db 1 UAGCGAGCACAUAAUGGUUUGUG 22

RESULT 2

ADA00122 ID ADA00122 standard; RNA; 22 BP.

XX AC ADA00122;

XX DT 0-NOV-2003 (first entry)

XX DE Mouse miRNA sequence miR-15a SEQ ID NO:119.
XX KW Drosophila melanogaster; human; mouse; microRNA; miRNA; cytostatic; gene therapy; diagnostic; therapeutic; developmental modulator; pathogenic modulator; cancer; B-cell chronic leukaemia; tissue reprogramming; ss.

XX OS Mus sp.

XX PN WO2003029459-A2.

XX PD 10-APR-2003.

XX XX 27-SEP-2002; 2002WO-EP010881.

XX PR 28-SEP-2001; 2001EP-00123453.

XX PR 22-MAR-2002; 2002EP-0006712.

XX PR 26-JUL-2002; 2002EP-0016772.

XX PA (PLAC) MAX PLANCK GES FOERDERUNG.

XX PT Tuschl T, Lagos-Quintana M, Lendeckel W, Meyer J, Rauhut R;

XX DR WPI; 2003-381637/36.

XX PT New nucleic acid molecule for diagnostic and therapeutic applications and as a marker or a modulator of developmental or pathogenic processes, e.g.

PT cancer, comprises microRNAs of a *Drosophila melanogaster*, a human or a mouse. XX PS Claim 1; Page 31; 138pp; English.

CC The present invention describes an isolated nucleic acid molecule (I) comprising a nucleotide sequence of *Drosophila melanogaster*, human or mouse microRNAs (miRNAs), or their precursors, a complement of it, a nucleotide sequence that has an affinity of at least 80% to them or a nucleotide sequence that hybridises under stringent conditions to them.

CC also described: (1) a pharmaceutical composition containing the nucleic acid and, optionally, a carrier; and (2) identifying miRNA molecules or precursor molecules, comprising ligating 5'- and 3'-adapter molecules to the ends of a size-fractionated RNA population, reverse transcribing the adapter-containing RNA population and characterising the reverse transcription products. (I) has cytostatic activity, and can be used in gene therapy. The pharmaceutical composition is useful for diagnostic and therapeutic applications, and as a marker or a modulator of developmental or pathogenic processes, particularly of cancer (e.g. B-cell chronic leukaemia) or gene expression. The miRNA molecules may also be used in tissue reprogramming procedures. The present sequence represents an miRNA sequence from the present invention.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 22; DB 8; Length 22; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCGAGCACAUAAUGGUUUGUG 22
Db 1 UAGCGAGCACAUAAUGGUUUGUG 22

RESULT 3

ADA017091 ID ADA017091 standard; RNA; 22 BP.

XX AC ADA017091;

XX DT 12-AUG-2004 (first entry)

XX DE Human miR15 processed RNA sequence SeqID3.

XX KW miR15; miR16; cancer; proliferation; cancer cell; cytostatic; gene therapy; chronic lymphocytic leukaemia; prostate cancer; micro RNA; chromosome 13q14; human; ss.

XX OS Homo sapiens.

XX PN WO2004043387-A2.

XX PD 27-MAY-2004.

XX PP 12-NOV-2003; 2003WO-US035777.

XX PR 13-NOV-2002; 2002US-0425844P.

PR 09-MAY-2003; 2003US-0469464P.

XX PA (UWJE-) UNIV JEFFERSON THOMAS.

XX PI Croce CN, Calin GA;

XX DR WPI; 2004-400825/37.

XX PT treating an miR15 or miR16 mediated cancer, i.e. chronic lymphocytic leukemia or prostate cancer, comprises administering to the subject an miR15 or miR16 gene product.

XX PS Claim 64; SEQ ID NO 3; 73pp; English.

CC This invention relates to a novel method of treating an miR15 or miR16 mediated cancer in a subject which comprises administering to the subject an amount of an isolated miR15 or miR16 gene product such that proliferation of miR15 or miR16 mediated cancer cells in inhibited. The miR15 and miR16 micro RNA genes are localised to 13q14 in humans, a region that is deleted in a significant portion of subjects suffering from chronic lymphocytic leukaemia or prostate cancer. The products of the miR15 and miR16 genes have also been found to inhibit the neoplastic or tumourigenic growth of chronic lymphocytic leukaemia or prostate cancer cells. The invention may be useful for the production of compounds with a cytostatic activity. In addition the invention may also be useful for gene therapy using the miR15 or miR16 gene product. The methods and

CC compositions are useful in diagnosing and treating miR15 or miR16
 CC mediated cancer, i.e. chronic lymphocytic leukaemia or prostate cancer.
 CC The present sequence is that of the human miR15 processed RNA sequence.
 CC which is used in the method of the invention.

XX SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCGGCAACAUAAUGGUUUGUG 22
 Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 4
 ADP84065
 ID ADP84065 standard; RNA; 22 BP.
 XX
 AC ADP84065;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Small nucleotide detection-related human miRNA SeqID2.
 XX
 KW small nucleic acid detection; interfering RNA; detection structure;
 KW miRNA; micro RNA; siRNA; short interfering RNA; human; ss.
 OS Homo sapiens.
 XX
 PN WO2004057017-A2.
 XX
 PD 08-JUL-2004.
 XX
 PP 18-DEC-2003; 2003WO-US041549.
 PR 18-DEC-2003; 2003US-00740256.
 XX
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 XX
 PT Dahlberg JE, Allawi HT, Iyamichev V, Neri BP, Olson-Munoz M;
 PT Chehak L, Olson SM;
 XX
 DR WPI; 2004-500306/17.
 XX
 PT Detecting small nucleic acids, such as miRNA and siRNA, by hybridizing an
 PT sequence not complementary to the interfering RNA target to generate a
 PT detection structure.
 XX
 PS Example 2; SEQ ID NO 62; 97pp; English.
 XX
 CC This invention relates to a novel method for modulating the expression of
 CC a target gene in a cell, for treating cancer, an
 CC a cell of a polynucleotide that forms a duplex region with an mRNA transcribed from
 CC transcribed from the target gene, where the duplex region comprises a
 CC mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that
 CC regulates mRNA at a post-transcriptional level. The present invention
 CC describes a method for controlling ontogenisis of a mammal, function of a
 CC mammalian cell, differentiation of a mammalian cell or viability of a
 CC mammalian cell in the post-transcriptional phase, which comprises
 CC introducing a plasmid vector comprising a promoter and nucleic acid
 CC molecule expressing an miRNA or siRNA silencing precursor to the mRNA.
 CC Accordingly, it provides a cell therapy method for treating cancer,
 CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,
 CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease
 CC by introducing into the cell the miRNA, siRNA silencing precursor to the
 CC mRNA or the plasmid vector. As such, they can be developed into
 CC pharmaceutical compositions that exhibit cytotoxic, immunosuppressive,
 CC neurotropic, neuroprotective and anti-inflammatory activities and hence can
 CC be used for immunotherapy. This oligonucleotide sequence is a human miRNA
 CC oligo that modulates expression of a target human gene, given in an
 CC exemplification of the invention.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
 Query Match 100.0%; Score 22; DB 13; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGGAGCACAUAAUGGUUUGUG 22
 Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 5
 ADR83121
 ID ADR83121 standard; RNA; 22 BP.
 XX
 AC ADR83121;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human miRNA oligo that modulates expression of human target mRNA Seq 23.
 XX
 KW human; ss; miRNA; microRNA; oncogenesis; cell therapy; cancer;
 KW immune disease; nerve disorder; amyotrophic lateral sclerosis;
 KW Parkinson's disease; Alzheimer's disease; inflammatory disease;
 KW siRNA silencing precursor; cytotoxic; immunosuppressive; nootropic;
 KW neuroprotective; antiinflammatory; immunotherapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004076622-A2.
 XX
 PD 10-SEP-2004.
 XX
 PP 10-FEB-2-2004; 2004WO-JP001433.
 XX
 PR 10-FEB-2003; 2003US-0445829P.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX
 PI Taira K, Kawasaki H;
 XX
 DR WPI; 2004-653393/63.
 XX
 PT Modulating expression of a target gene in a cell, for treating cancer, an
 PT immune disease, or a nerve disorder, comprises introducing into the cell
 PT a polynucleotide that forms a duplex region with an mRNA transcribed from
 PT the target gene.
 XX
 PS Claim 6; SEQ ID NO 23; 865pp; English.

CC This invention relates to a novel method for modulating the expression of
 CC a target gene in a cell. Specifically, it refers to the introduction into
 CC a cell of a polynucleotide that forms a duplex region with an mRNA
 CC transcribed from the target gene, where the duplex region comprises a
 CC mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that
 CC regulates mRNA at a post-transcriptional level. The present invention
 CC describes a method for controlling ontogenisis of a mammal, function of a
 CC mammalian cell, differentiation of a mammalian cell or viability of a
 CC mammalian cell in the post-transcriptional phase, which comprises
 CC introducing a plasmid vector comprising a promoter and nucleic acid
 CC molecule expressing an miRNA or siRNA silencing precursor to the mRNA.
 CC Accordingly, it provides a cell therapy method for treating cancer,
 CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,
 CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease
 CC by introducing into the cell the miRNA, siRNA silencing precursor to the
 CC mRNA or the plasmid vector. As such, they can be developed into
 CC pharmaceutical compositions that exhibit cytotoxic, immunosuppressive,
 CC neurotropic, neuroprotective and anti-inflammatory activities and hence can
 CC be used for immunotherapy. This oligonucleotide sequence is a human miRNA
 CC oligo that modulates expression of a target human gene, given in an
 CC exemplification of the invention.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 22; DB 13; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGGAGCACAUAAUGGUUUGUG 22
 Db 1 UAGCAGCACAUAAUGGUUUGUG 22

XX New oligomeric compound that can hybridize with or sterically interfere
 PT with nucleic acid molecules comprising or encoding small non-coding RNA
 PT targets, useful for treating e.g., cancer and diabetes.

XX Example 4; SEQ ID NO 269; 854pp; English.

CC The invention relates to an oligomeric compound comprising a first region
 CC and a second region, where at least one region contains a modification,
 CC and a portion of the oligomeric compound is targeted to a small non-
 CC coding RNA target nucleic acid that is miRNA (micro-RNA), or its
 CC precursor (primary-miRNA, pri-miRNA). Also included are a composition
 CC comprising a first oligomeric compound and a second oligomeric compound
 CC (where at least one of the oligomeric compounds contains a modification,
 CC at least a portion of the first oligomeric compound is capable of
 CC hybridizing with at least a portion of the second oligomeric compound,
 CC and at least a portion of the first oligomeric compound is targeted to a
 CC small non-coding RNA target nucleic acid, a pharmaceutical composition
 CC comprising the composition cited above (and a carrier), a kit or assay
 CC devic comprising the composition, modulating the expression of a small
 CC non-coding RNA target nucleic acid in a cell (or tissue or animal),
 CC treating or preventing a disease or disorder associated with a small non-
 CC coding RNA target nucleic acid, treating a condition in an animal,
 CC treating or preventing a disease or disorder associated with CD36,
 CC methods of screening an oligomeric compound for an effect on miRNA
 CC signaling, methods of modulating translation (or apoptosis, conversion of
 CC a precursor miRNA into miRNA, or cellular differentiation), identifying
 CC an RNA transcript bound to a small non-coding RNA, arresting (or
 CC delaying) entry of a cell into the G2/M phase, interfering with chromosome
 CC segregation, a method of triggering apoptosis, detecting a miRNA
 CC precursor, identifying a miRNA target, modulating cellular
 CC differentiation, treating a condition associated with adipocyte
 CC associated with aberrant regulation of the cell cycle by miRNAs,
 CC maintaining a pluripotent stem cell and identifying a small non-coding
 CC RNA binding site. The oligomeric compound is targeted to a region
 CC flanking a Drosophila cleavage site within a pri-miRNA. It stimulates an
 CC increase in expression of a pri-miRNA. The compounds and compositions are
 CC useful for treating a disease or disorder resulting from chromosomal non-
 CC disjunction, altered methylation, acetylation, or pseudouridylation state
 CC of chromosomes, such as a hyperproliferative condition (e.g. cancer,
 CC neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
 CC hyperlipidemia, atherosclerosis, heterogeneity, hypertension, anorexia,
 CC Alzheimer's disease, a central nervous system injury or neurodegenerative
 CC disorder. The present sequence is a mature miRNA of the invention.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

XX Query Match 100.0%; Score 22; DB 14; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAAUGGUUUGUG 22

Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 8

ID ADY30915 standard; DNA; 22 BP.

AC ADY30915;

DT 05-MAY-2005 (first entry)

XX Micro RNA (miRNA)-related DNA targeted to human E2F3/EIF5A2/FOXA1 -SEQ 7.

XX miRNA; micro RNA; RNA interference; gene silencing;

XX E2F transcription factor 3; E2F3;

XX eukaryotic translation initiation factor 5A2; EIF5A2; forkhead box A1;

XX FOXA1; hepatocyte nuclear factor 3 alpha; HNF3alpha; ss.

OS Homo sapiens.

XX WO2005017145-A1.

PR 13-AUG-2003; 2003JP-00293129.

XX (NIBI-) JAPAN BIOLOGICAL INFORMATICS CONSORTIUM.

PA (BITS-) BITS CO LTD.

PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX Barrero Roberto Antonio, Tamura T, Imanishi T, Gojobori T;

PI Taira K, Kawasaki H;

XX DR WPI: 2005-196094/20.

XX PS Claim 8; SEQ ID NO 7; 38pp; Japanese.

CC The invention relates to a novel method for identifying or presuming a
 CC functional miRNA (micro RNA) molecule of base length of 16-25 and a gene
 CC which is regulated as a result of targeting by the miRNA. The method
 CC comprises determining and classifying the base sequences of functional
 CC RNA molecules into conserved and unconserved regions, setting ambiguities
 CC of different standards in these regions and searching for a candidate
 CC gene which has a base sequence complementary to the functional RNA
 CC molecule. The method of the invention may be useful for identifying a
 CC gene whose expression is under regulation by a functional RNA molecule of
 CC base length of 16-25. The method is thus useful for developing treatments
 CC for a disease or for treating a disease by controlling the biological
 CC function of the target gene. The current sequence is that of a micro RNA
 CC (miRNA)-related DNA of the invention which is targeted to a human gene.
 CC Specifically, human E2F transcription factor 3 (E2F3), eukaryotic
 CC translation initiation factor 5A2 (EIF5A2) and forkhead box A1 (FOXA1,
 CC hepatocyte nuclear factor 3 alpha, HNF3alpha) are referred to in claim 9.

XX Sequence 22 BP; 6 A; 3 C; 6 G; 7 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 22; DB 14; Length 22;
 Best Local Similarity 68.2%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAAUGGUUUGUG 22

Db 1 TAGCAGCACATAAAGGTTTG 22

RESULT 9

ID ADX85423 standard; RNA; 22 BP.

AC ADX85423;

XX DT 05-MAY-2005 (first entry)

XX DE Human/mouse miR-15 microRNA that binds hOMP1 target mRNA.

XX miRNA recognition element; MRE; bioinformatics; gene expression; ss.

XX OS Homo sapiens.

OS Mus sp.

XX Key Location/Qualifiers

FT misc_binding 1..17 /*tag= a

FT /bound_moiety= "hOMP1 MRE"

FT /note= "Forms double stranded region with nucleotides 17-
 FT 1"
 FT
 XX WO2005017111-A2.
 XX
 XX PD 24-FEB-2005.
 XX
 XX PF 15-JUL-2004; 2004WO-US022934.
 XX
 PR 15-JUL-2003; 2003US-0487321P.
 XX
 PA (UYRE-) UNIV PENNSYLVANIA.
 XX
 PT Hatzigeorgiou AG, Mourikos Z;
 XX
 DR WPI; 2005-182352/19.
 XX
 PT Identifying a microRNA-recognition element by comparing the degree of
 PT complementarity of a microRNA nucleotide sequence to an mRNA sequence.
 XX
 PS Example 1; FIG 6; 51pp; English.
 XX
 CC This invention relates to a novel method for identifying a microRNA-
 CC recognition element (MRE). Specifically, it refers to comparing the
 CC degree of complementarity of a microRNA nucleotide sequence (mRNA) to an
 CC mRNA target sequence in order to identify the presence of a sequence that
 CC is indicative of an MRE for the microRNA. In particular, it refers to
 CC microRNA-MRE recognition rules that allow prediction of human and mouse
 CC mRNA targets. The present invention also describes determining the free
 CC energy of the microRNA bound to the selected 3' untranslated region of an
 CC mRNA sequence i.e. the MRE sequence. Furthermore, it provides an
 CC oligonucleotide that is synthesized having the sequence of the generated
 CC microRNA and contacting the microRNA with a cell expressing the mRNA in
 CC order to down regulate expression of that mRNA. It describes a system for
 CC identifying a microRNA-recognition element as comprising an interface for
 CC inputting mRNA sequences, a database of mRNA sequences or a link for
 CC connecting to a remote data input interface, data or a database of mRNA
 CC sequences and a processor with instructions for comparing mRNA sequences
 CC to microRNA sequences to identify an MRE. This oligonucleotide is a
 CC human/ mouse microRNA sequence that binds to a microRNA-recognition
 CC element of the target mRNA given in an exemplification of the invention.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 22; DB 14; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAGAAUGGUUGUG 22
 Db 1 UAGCAGCACAGAAUGGUUGUG 22

RESULT 10

ADZ20390
 ID ADZ20390 standard; RNA; 22 BP.
 AC ADZ20390;
 XX
 DT 16-JUN-2005 (first entry)

DE Human hematopoietic miRNA, miR-15a B1_F06-2, SEQ ID NO: 9 #2.
 XX
 KW Expression; gene therapy; hematological disease; cancer; infection;
 KW cytostatic; antibacterial; viricide; fungicide; antimicrobial; neoplasm;
 KW ss; micro RNA; miRNA.
 XX
 OS Homo sapiens.
 XX
 US2005075492-A1.
 XX
 PD 07-APR-2005.
 XX

RESULT 11

ADZ36205
 ID ADZ36205 standard; RNA; 22 BP.
 AC ADZ36205;
 DT 03-NOV-2005 (first entry)

DB Nucleotide sequence of known human miRNA #9.

XX RNA interference; gene silencing; microRNA; miRNA; gene therapy;
 KW Huntingtons chorea; cardiovascular disease; cardiovascular-gen.;
 KW immune disorder; immunomodulator; liver disease; hepatotropic;
 KW gastrointestinal disease; viral infection; viricide; infection; pain;
 KW analgesic; neurological disease; metabolic disorder; metabolic;
 KW metabolic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 WO2005078096-A2.
 XX
 PD 25-AUG-2005.
 XX
 PF 09-FEB-2005; 2005WO-US04206.
 XX
 PR 09-FEB-2004; 2004US-0543467P.
 XX
 PA (UTMA-) UNIV MASSACHUSETTS.

PP 06-AUG-2004; 2004US-00913288.
 XX
 PR 07-AUG-2003; 2003US-0493239P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Chen C, Bartel D, Iodish H;
 XX
 DR WPI; 2005-283812/29.
 XX
 PT New precursor microRNA molecule comprises isolated nucleic acid
 PT comprising a stem-loop structure and a microRNA flanking sequence, useful
 PT for treating hematopoietic disorders including cancers, viral, bacterial,
 PT or fungal infections.
 XX
 PS Disclosure; SEQ ID NO 9; 39pp; English.
 XX
 CC The present invention relates to a precursor microRNA (miRNA) molecule
 CC comprising a stem-loop structure and a microRNA flanking sequence. The
 CC invention also provides a method for producing miRNA. The invention is
 CC useful for treating hematopoietic disorders including cancers, e.g.
 CC leukemia, lymphoma, or rectal cancer and infections, e.g. viral, bacterial,
 CC prostate cancer, or brain cancer, head and neck cancer,
 CC or fungal infections. The precursor miRNA is useful for regulating the
 CC expression of protein-coding genes at the posttranscriptional level and
 CC also be used as therapeutics and as research tools, e.g. analyzing gene
 CC function. The invention is useful in gene therapy. The present sequence
 CC is the human hematopoietic miRNA plays a role in hematopoiesis. The
 CC current sequence is that of the human miRNA which is located on
 CC chromosome 13q13.3. Note: The present sequence is the SEQ ID NO: 9 which
 CC is shown on page 7. This sequence differs from the SEQ ID NO: 9 given in
 CC the sequence listing (see ADZ20370).
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
 Query Match 100.0%; Score 22; DB 14; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAGAAUGGUUGUG 22
 Db 1 UAGCAGCACAGAAUGGUUGUG 22

DR XX
 PI XX
 PT XX
 PT XX
 PT XX
 PT XX
 PS Disclosure; Page 11; 80pp; English.

The specification describes a RNA-silencing agent, comprising an mRNA targeting moiety, a linking moiety, a recruiting moiety, and a microRNA (miRNA) recruiting moiety. The RNA-silencing agent of the invention is useful for repressing translation of a target mRNA for treating Huntington's disease.

XX
 XX
 CC targeting moiety, a linking moiety, and a microRNA (miRNA) recruiting moiety. The RNA-silencing agent of the invention is useful for the manufacture of medicament for repressing mutant gene expression, such as Huntington's disease in this manner. The agent may also be useful in the treatment of one or more of cellular proliferative and/or differentiative disorders, cardiovascular disorders, immune disorders, hematopoietic disorders, liver disorders, viral diseases, pain or metabolic disorders. ABC36197-ABC36300 represent known human miRNAs.

XX
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100%; Score 22; DB 14; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 UAGCAGCACAUAAUGGUUGUG 22
 DB 1 UAGCAGCACAUAAUGGUUGUG 22

RESULT 12

ABD3521
 ID ABD35921 standard; DNA; 22 BP.
 XX
 AC ABD35921;
 XX
 DT 15-DEC-2005 (first entry)
 XX
 DE Hsa-miR-15a DNA target.
 XX
 KW RNA interference; RNA purification; RNA amplification; gene silencing;
 XX RNA detection; micro RNA; miRNA; miR-15a; ss.
 XX OS Homo sapiens.
 XX
 FT Location/Qualifiers
 FT modified_base 22
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 3" Phosphorylated"
 XX
 WO2005098029-A2.
 XX
 PDD 20-OCT-2005.
 XX
 PP 07-APR-2005; 2005WO-DK0000239.
 XX
 PR 07-APR-2004; 2004DK-00000578.
 PR 23-JUL-2004; 2004DK-00001146.
 PR 11-AUG-2004; 2004DK-00001218.
 PR 15-OCT-2004; 2004DK-00001587.
 PR 28-JAN-2005; 2005DK-00000140.
 XX
 PA (EXIQ-) EXIQON AS.
 XX
 PT Jacoben N, Kongsbak L, Kauppinen S, Eichwald SM, Mouritzen P;
 PT Nielsen PS, Norholm M;
 XX
 DR WPI; 2005-714540/73.

PT Isolating, purifying, amplifying, detecting, identifying, quantifying or

PR 23-JUL-2004; 2004DK-0000146.
 PR KW RNA interference; RNA purification; RNA amplification; gene silencing;
 11-AUG-2004; 2004DK-00001218.
 PR KW RNA detection; micro RNA; miRNA; miR-15a; ss.
 PR 15-OCT-2004; 2004DK-00001587.
 PR 28-JAN-2005; 2005DK-0000140.
 XX PA (EXIQ-) EXIQON AS.
 XX ID Jacobson N, Kongbak L, Kauppinen S, Ehwald SM, Mouritzen P;
 PI Nielsen PS, Norholm M;
 XX DR WPI; 2005-714540/73.
 XX PT Isolating, purifying, amplifying, detecting, identifying, quantifying or
 capturing non-coding RNAs such as micro RNA or small interfering RNA
 (siRNA), involves using oligonucleotide containing nucleoside analogs.
 XX PT (siRNA), involves using oligonucleotide containing nucleoside analogs.
 XX PS Example; Page 69; 180PP; English.
 XX CC The present invention relates to the use of an oligonucleotide for the
 isolation, purification, amplification, detection, identification, quantification or
 capture of microRNA (miRNA) or small interfering RNA (siRNA), where the oligonucleotide contains a number of nucleoside
 analogs, e.g. locked nucleic acid (LNA), for sensitive and specific hybridization to
 analogs. The method uses 2 anchored tagging probes, each designed in
 combination to detect a complementary target sequence, e.g. a short RNA
 sequence, where the first tagging probe hybridizes to a first region
 within a target sequence and the second tagging probe hybridizes to a
 second region within the same complementary target sequence, e.g. a short
 RNA target sequence that is adjacent to the first region. In a preferred
 mode, one of the tagging probes is 5', phosphorylated to enable covalent
 coupling of the 2 contiguous tagging probes hybridized to the
 complementary target sequence by a ligase to form a single
 oligonucleotide sequence. The method takes advantage of substitution of
 the recognition sequences with high-affinity nucleotide analogs, e.g.
 locked nucleic acid (LNA), for sensitive and specific hybridization to
 short target sequences, e.g. miRNAs or siRNAs. The ligation reaction is
 followed by real-time quantitative PCR (qPCR) of the target sequence,
 priming sites for the PCR primers and a short detection probe with
 sufficient duplex stability to allow binding to the amplicon, and
 employing any of a variety of detection principles used in homogeneous
 assays. In the preferred mode, the detection probe is substituted with
 e.g. ribonucleic acid-templated, covalently joined oligonucleotide
 molecules using anchor sequences attached to the tagging probes as
 priming sites for the PCR primers and a short detection probe with
 sufficient duplex stability to allow binding to the amplicon, and
 duplex-stabilizing, high-affinity nucleotide analogs, e.g. LNA, and
 preferably oxy-LNA, to allow the use of short detection probes in the
 real-time qPCR. The method is useful for detecting and quantifying
 individual small RNA molecules in complex mixtures of different nucleic
 acids, and for detecting, testing, diagnosing or quantifying miRNAs,
 siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative mRNA
 splice variants implicated in, or connected to, human disease in complex
 nucleic acid samples, e.g. from cancer patients. The present sequence is
 that of human miR-15a RNA, which was used as a target sequence in a real-
 time qPCR assay of human miR-15a in an example from the invention.
 XX SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
 XX Query Match 100.0%; Score 22; DB 14; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX OY 1 UAGCCGGCACAUAAUGGUUUG 22
 Db 1 UAGCAGCACAUAAUGGUUUG 22
 XX DE Human micro RNA miR-15a.
 RESULT 14
 AED35991
 ID AED35991 standard; RNA; 22 BP.
 XX SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
 XX Query Match 100.0%; Score 22; DB 14; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX OY 1 UAGCAGCACAUAAUGGUUUG 22

Db 1 ||||||| UAGCAGCACAUAAUGGUUUGUG 22

RESULT 15
AED53385
ID AED53385 standard; RNA; 22 BP.
XX
AC AED53385;
XX
DT 29-DEC-2005 (first entry)

DB Human target / micro RNA oligo, hsa-mir-15.

XX KW RNA interference; micro RNA; miRNA; transcription; gene regulation;
KW microarray; ss.
XX OS Homo sapiens.

XX PN JP2005296014-A.

XX PD 27-OCT-2005.

XX PF 06-APR-2005; 2005US-00109915.

XX PR 06-APR-2004; 2004US-00118956.

XX PA (EPPE-) EPPENDORF ARRAY TECHNOLOGIES SA.

XX PI Van Veffter C, Lemacre J, Bulov S, Samatheo N;

XX DR WPI; 2005-753146/77.

XX PT Determining RNA interference mediated transcriptional regulation of cell, by ligting RNA of cell to polynucleotide by which target was labeled and hybridizing it to probe for transcription material, in array, PT detecting signal.

XX PS Claim 31; Page 20; 30PP; Japanese.

XX The invention relates to a novel method for determining RNA interference (RNAi) mediated transcriptional regulation of a cell, by determining patterns of at least 3 micro RNAs (miRNAs). The method involves preparing an array with capture probe of transcription material from the DNA of a cell, isolating an miRNA pool existing latently from the cell, extending the miRNA or ligating it to a polynucleotide with a labeled target, hybridizing the polynucleotide with a probe in an array and detecting a signal from the array. The invention further includes a kit for carrying out the above method. The method is useful for determining RNAi mediated transcriptional regulation of a cell. This sequence represents a human target / miRNA oligo for use in a microarray of the invention.

XX SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
Db 1 ||||||| UAGCAGCACAUAAUGGUUUGUG 22

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Job time : 107.39 secs

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OM nucleic - nucleic search, using SW model

Run on: November 1, 2006, 20:59:58 ; Search time 38.1333 seconds

1079.486 Million cell updates/sec

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Gapext 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query

Match Length DB ID

Description

TYPE: DNA

ORGANISM: Human

US-09-949-016-76948

Sequence 76948, A
Sequence 15525, A
Sequence 17202, A
Sequence 13978, A

Query Match 78.2%; Score 17.2%; DB 3; Length 601;

Best Local Similarity 59.1%; Pred. No. 72; Mismatches 3; Indels 0; Gaps 0;

Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Sequence 110759, Sequence 11090, Sequence 11081, Sequence 111242, Sequence 5921, AP Sequence 1, AP1 Sequence 1, AP11

Sequence 1, AP11 Sequence 252, APD Sequence 14810, A Sequence 14811, A Sequence 14880, A Sequence 14812, A Sequence 14813, A Sequence 17630, A Sequence 36194, A Sequence 54602, A Sequence 54634, A Sequence 54666, A Sequence 119031, Sequence 119031,

RESULT 1

US-09-949-016-76948

; Sequence 76948, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 76948

LENGTH: 601

ALIGNMENTS

RESULT 2
US-09-949-016-15525

; Sequence 15525, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 76948

LENGTH: 601

24 16.6 75.5 601 3 US-09-949-016-119067 Sequence 119067,
25 16.6 75.5 601 3 US-09-949-016-119103 Sequence 119103,
26 16.6 75.5 601 3 US-09-949-016-119139 Sequence 119139,
27 16.6 75.5 601 3 US-09-949-016-119175 Sequence 119175,
28 16.6 75.5 601 3 US-09-949-016-119211 Sequence 119211,
29 16.4 74.5 1365 3 US-09-949-016-2063 Sequence 2063, AP
30 16.4 74.5 6946 3 US-09-949-016-13805 Sequence 13805, A
31 16.2 73.5 601 3 US-09-949-016-46039 Sequence 46039, AP
32 16.2 73.6 601 3 US-09-949-016-92412 Sequence 9412, A
33 16.2 73.6 601 3 US-09-949-016-137903 Sequence 137903,
34 16.2 73.5 777 3 US-09-956-178-1156 Sequence 1156, AP
35 16.2 73.6 777 3 US-08-781-9861-1156 Sequence 4772, AP
36 16.2 73.5 1140 3 US-09-248-7962-4772 Sequence 4660, AP
37 16.2 73.5 1771 3 US-09-248-7962-4660 Sequence 5, Appl. 1
38 16.2 73.6 4880 3 US-09-402-929-5 Patent No. 5175383
39 16.2 73.6 7868 10 5175383-1, Sequence 19, Appl. Sequence 1224, A
40 16.2 73.5 43572 3 US-09-676-519-19 Sequence 15618, A
41 16.2 73.6 52711 3 US-09-949-016-12224 Sequence 16267, A
42 16.2 73.6 52865 3 US-09-949-016-15618 Sequence 14385, A
43 16.2 73.6 54531 3 US-09-949-016-14385 Sequence 13058, A
44 16.2 73.6 72602 3 US-09-949-016-13058

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 15525
; LENGTH: 117807
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15525

Query Match 78.2%; Score 17.2; DB 3; Length 117807;
Best Local Similarity 59.1%; Pred. No. 1.5e+02; Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 1 UAGCAGCACAUAAUGGUUGUG 22
Db 29126 TAGCATCATATGGCTGTG 29147

RESULT 3
US-09-949-016-17202
; Sequence 17202, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 17202
; LENGTH: 189560
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO: 189560
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11..(236341))
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-13978

Query Match 78.2%; Score 17.2; DB 3; Length 236341;
Best Local Similarity 59.1%; Pred. No. 1.7e+02; Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 1 UAGCAGCACAUAAUGGUUGUG 22
Db 187064 TAGAGGCAACAAATGGTTGTG 187043

RESULT 5
US-09-949-016-110759
; Sequence 110759, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 110759
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-110759

Query Match 76.4%; Score 16.8; DB 3; Length 601;
Best Local Similarity 65.0%; Pred. No. 1.1e+02; Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 1 UAGCAGCACAUAAUGGUUGUG 20
Db 398 TAGCAGCACATAATGCTATG 417

RESULT 6
US-09-949-016-110920
; Sequence 110920, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

```

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; SEQ ID NO 111242
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-111242

Query Match 76.4%; Score 16.8; DB 3; Length 601;
Best Local Similarity 65.0%; Pred. No. 1.1e+02; Mismatches 2;
Matches 13; Conservative 5; MisMatches 2; Indels 0; Gaps 0;
Qy 1 UAGCAGCACAUAAUGGUUG 20
Db 398 TAGCAGCACATAATGCTATG 417

RESULT 7
US-09-949-016-111081 Application US/09949016
; Sequence 111081, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016

CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 6/0/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 6/0/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 6/0/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO 111081
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-111081

Query Match 76.4%; Score 16.8; DB 3; Length 601;
Best Local Similarity 65.0%; Pred. No. 1.1e+02; Mismatches 2;
Matches 13; Conservative 5; MisMatches 2; Indels 0; Gaps 0;
Qy 1 UAGCAGCACAUAAUGGUUG 20
Db 398 TAGCAGCACATAATGCTATG 417

RESULT 9
US-09-248-796A-5921/C
; Sequence 5921, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:
; APPLICANT: Keith Wainstock et al
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 101196-132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; PRIOR APPLICATION NUMBER: US 60/074, 725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096, 409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5921
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Candida albicans
; US-09-248-796A-5921

Query Match 76.4%; Score 16.8; DB 3; Length 966;
Best Local Similarity 60.0%; Pred. No. 1.2e+02; Mismatches 2;
Matches 12; Conservative 6; MisMatches 2; Indels 0; Gaps 0;
Qy 3 GCACCAACAUAAUGGUUG 22
Db 734 GCAGCAAAATAATGTTGTCG 715

RESULT 10
US-09-070-356-1/C
; Sequence 1, Application US/09070356
; Patent No. 6226631

GENERAL INFORMATION:
; APPLICANT: Alex Zhu
; APPLICANT: Jack Goldstein
; TITLE OF INVENTION: Recombinant  $\alpha$ -N-Acetylglucosaminidase
; TITLE OF INVENTION: Acetylglucosaminidase
; TITLE OF INVENTION: Enzyme and cDNA Encoding
; NUMBER OF SEQIDNOS: 7

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amster, Rothstein & Eberstein
; STREET: 90 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10016

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.4 Mb storage diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070, 356
; FILING DATE: US/09/070, 356

```

CLASSIFICATION: PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/037,248
 FILING DATE: March 26, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pasqualini, Patricia A.
 REFERENCE/DOCKET NUMBER: 34,894
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 697-5995
 TELEX: TWX 710-581-4766
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2319
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 DESCRIPTION: cDNA to mRNA
 HYPOTHETICAL: no
 ANTI-SENSE: yes
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: chicken liver
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HARLOTYPE:
 TISSUE TYPE:
 CELL TYPE:
 CELL LINE:
 ORGANELLE:
 IMMEDIATE SOURCE: library
 POSITION IN GENOME: unknown
 CHROMOSOME/SEGMENT:
 MAP POSITION:
 UNITS:
 FEATURE:
 NAME/KEY: chicken liver a-N-acetylgalactosaminidase
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 ; US-09-356-1

RESULT 11
 US-08-406-070-1/C
 Sequence 1, Application US/08406070
 ; Sequence 1, Application US/08406070
 ; Patent No. 5611063
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Daniel S.
 ; ATTORNEY: Walker, John C.
 ; APPLICANT: Walker, John C.
 ; US-09-356-1

Query Match 76.4%; Score 16.8; DB 3; Length 2319;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02; Mismatches 22;
 Matches 12; Conservative 6; Missmatches 2; Indels 0; Gaps 0;
 QY 3 GCAGCACAUAAUGGAGUUG 22
 Db 670 GCAGCACATCCGTTG 651

RESULT 12
 US-09-356-1/C
 Sequence 252, Application US/09984429
 ; Sequence 252, Application US/09984429
 ; Patent No. 702647
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 53 Human Secreted Proteins
 FILE REFERENCE: P2018P2
 CURRENT APPLICATION NUMBER: US/09/984,429
 CURRENT FILING DATE: 2001-10-30
 PRIOR APPLICATION NUMBER: 60/244,591
 PRIOR FILING DATE: 2000-11-01
 PRIOR APPLICATION NUMBER: 09/288,143
 PRIOR FILING DATE: 1999-04-08
 PRIOR APPLICATION NUMBER: PCT/US98/21142
 PRIOR FILING DATE: 1998-10-08
 PRIOR APPLICATION NUMBER: 60/061,463
 PRIOR FILING DATE: 1997-10-09
 PRIOR APPLICATION NUMBER: 60/061,529
 PRIOR FILING DATE: 1997-10-09
 PRIOR APPLICATION NUMBER: 60/071,498
 PRIOR FILING DATE: 1997-10-09
 PRIOR APPLICATION NUMBER: 60/061,527
 PRIOR FILING DATE: 1997-10-09
 PRIOR APPLICATION NUMBER: 60/061,536
 PRIOR FILING DATE: 1997-10-09

TITLE OF INVENTION: A cDNA For
 TITLE OF INVENTION: alpha-N-acetyl-galactosaminidase From Gallus domesticus
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
 STREET: P. O. Box 4390
 CITY: Troy
 STATE: Michigan
 COUNTRY: US
 ZIP: 48099
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/406,070
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kohn, Kenneth I.
 REGISTRATION NUMBER: 30 955
 REFERENCE/DOCKET NUMBER: UMO P-317
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (810) 689-3500
 TELEX: (810) 689-4071
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2334 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 2315..2334

US-08-406-070-1

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; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 43991
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-984-429-252

Query Match 76.4%; Score 16.8; DB 5; Length 43991;
Best Local Similarity 65.0%; Pred. No. 2..e+02; Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 1 UAGCAGCACAUAAUGGUUG 20
Db 10240 TAGCAGAACACATGGTG 10259

RESULT 13
US-09-949-016-14810
; Sequence 14810, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14810
; LENGTH: 174170
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(174170)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-14810

Query Match 76.4%; Score 16.8; DB 3; Length 174170;
Best Local Similarity 65.0%; Pred. No. 2.5e+02; Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 1 UAGCAGCACAUAAUGGUUG 20
Db 56392 TAGCAGAACACATGGTG 56391

RESULT 14
US-09-949-016-14811
; Sequence 14811, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14811
; LENGTH: 174318
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(174318)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-14811

Query Match 76.4%; Score 16.8; DB 3; Length 174318;
Best Local Similarity 65.0%; Pred. No. 2.5e+02; Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 1 UAGCAGCACAUAAUGGUUG 20
Db 56520 TAGCAGAACACATGGTG 56539

RESULT 14
US-09-949-016-14811
; Sequence 14811, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14811
; LENGTH: 174318
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(174318)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-14811

Query Match 76.4%; Score 16.8; DB 3; Length 174318;
Best Local Similarity 65.0%; Pred. No. 2.5e+02; Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 1 UAGCAGCACAUAAUGGUUG 20
Db 56520 TAGCAGAACACATGGTG 56539

Search completed: November 1, 2006, 22:24:17
Job time : 44.133 sec

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 22:20:01 ; Search time 527.371 Seconds
(without alignments)
512.595 Million cell updates/sec

Title: US-10-706-798-3
Perfect score: 22
Sequence: 1 uagcagcacauaauugguug 22

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Gapop 10.0 , Gapext 1.0
Searched: 18892170 seqs, 6143817638 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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2: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US08_PUBCOMB.seq: *
3: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US09A_PUBCOMB.seq: *
4: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US09C_PUBCOMB.seq: *
5: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US10A_PUBCOMB.seq: *
6: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US10B_PUBCOMB.seq: *
7: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US10C_PUBCOMB.seq: *
8: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US10D_PUBCOMB.seq: *
9: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US10E_PUBCOMB.seq: *
10: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US10F_PUBCOMB.seq: *
11: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US10G_PUBCOMB.seq: *
12: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US11A_PUBCOMB.seq: *
13: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US11B_PUBCOMB.seq: *
14: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US11C_PUBCOMB.seq: *
15: /EMC_Celerra_SIDS3/ptodata/2/pupbna/US11D_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

RESULT 1
US-10-706-798-3
; Sequence 3. Application US/10706798
; Publication No. US20040152112A1.
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Cain, George A.
; TITLE OF INVENTION: Compositions and Methods for Cancer
; TITLE OF INVENTION: Diagnosis and Therapy
; FILE REFERENCE: 08211-0126US1
; CURRENT APPLICATION NUMBER: US/10/706,798
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,864
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/469,464
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-706-798-3

Query Match 100.0%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9%;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 UAGCAGCACAUUAGGUUGUG 22

Dy 1 UAGCAGCACAUUAGGUUGUG 22

Sequence 1, Appli
Sequence 248, Appli
Sequence 305, Appli
Sequence 72, Appli
Sequence 1, Appli
Sequence 128, Appli
Sequence 165, Appli
Sequence 96, Appli
Sequence 19, Appli
Sequence 1151, Appli
Sequence 1768, Appli
Sequence 23, Appli
Sequence 6557, Appli
Sequence 6769, Appli
Sequence 77545, Appli
Sequence 5, Appli
Sequence 1115, Appli
Sequence 1886, Appli
Sequence 120, Appli
Sequence 449, Appli
Sequence 246, Appli
Sequence 345, Appli
Sequence 112, Appli
Sequence 132, Appli
Sequence 306, Appli
Sequence 1286, Appli
Sequence 2, Appli
Sequence 80, Appli

;

```

; APPLICANT: Lendeckel, Winfried
; APPLICANT: Meyer, Jutta
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2923-613
; CURRENT APPLICATION NUMBER: US/10/490, 955
; CURRENT FILING DATE: 2004-03-29
; PRIORITY APPLICATION NUMBER: PCT/EP02/10881
; PRIORITY FILING DATE: 2002-09-27
; PRIORITY APPLICATION NUMBER: EP 02 015 772.2
; PRIORITY FILING DATE: 2002-07-26
; PRIORITY APPLICATION NUMBER: EP 02 006 712.0
; PRIORITY FILING DATE: 2002-03-22
; PRIORITY APPLICATION NUMBER: EP 01 123 453.1
; PRIORITY FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 81
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-490-955-81

RESULT 3
Query Match 100.0%; Score 22; DB 10; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 UAGCAGCACAAUAGUAGUUG 22
Db 1 UAGCAGCACAAUAGUAGUUG 22

US-10-490-955-119
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 UAGCAGCACAAUAGUAGUUG 22
Db 1 UAGCAGCACAAUAGUAGUUG 22

RESULT 4
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 UAGCAGCACAAUAGUAGUUG 22
Db 1 UAGCAGCACAAUAGUAGUUG 22

RESULT 5
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 UAGCAGCACAAUAGUAGUUG 22
Db 1 UAGCAGCACAAUAGUAGUUG 22

US-10-490-955-448
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 UAGCAGCACAAUAGUAGUUG 22
Db 1 UAGCAGCACAAUAGUAGUUG 22

US-10-490-955-62
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 UAGCAGCACAAUAGUAGUUG 22
Db 1 UAGCAGCACAAUAGUAGUUG 22

US-10-490-955-22
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 UAGCAGCACAAUAGUAGUUG 22
Db 1 UAGCAGCACAAUAGUAGUUG 22

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QY 1 UAGCAGCACAUAAUGGUUUG 22
 US-10-909-125-269
 ; Sequence 269, Application US/10909125
 ; Publication No. US20050261218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Esau, Christine
 ; APPLICANT: Lollo, Bridget
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Freier, Susan M.
 ; APPLICANT: Griffey, Richard H.
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: Vickers, Timothy
 ; APPLICANT: Marcussen, Eric G.
 ; APPLICANT: Koller, Erich
 ; APPLICANT: Swayze, Eric
 ; APPLICANT: Jain, Ravi
 ; APPLICANT: Bhat, Balkrishen
 ; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
 ; TITLE OF INVENTION: Of Small Non-Coding RNAs
 ; FILE REFERENCE: US10080-100 (CORE016US)
 ; CURRENT APPLICATION NUMBER: US/10/909,125
 ; CURRENT FILING DATE: 2004-07-30
 ; PRIOR APPLICATION NUMBER: US 60/492,056
 ; PRIOR FILING DATE: 2003-07-31
 ; PRIOR APPLICATION NUMBER: US 60/516,303
 ; PRIOR FILING DATE: 2003-10-31
 ; PRIOR APPLICATION NUMBER: US 60/531,596
 ; PRIOR FILING DATE: 2003-12-19
 ; PRIOR APPLICATION NUMBER: US 60/562,417
 ; CURRENT FILING DATE: 2004-04-14
 ; NUMBER OF SEQ ID NOS: 2184
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 269
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: H. sapiens
 ; US-10-909-125-269

Query Match 100.0%; Score 22; DB 10; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; APPLICANT: Esau, Christine
 QY 1 UAGCAGCACAUAAUGGUUUG 22
 Db 1 UAGCAGCACAUAAUGGUUUG 22

RESULT 7
 US-10-909-125-369/C
 ; Sequence 369, Application US/10909125
 ; Publication No. US20050261218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Esau, Christine
 ; APPLICANT: Lollo, Bridget
 ; APPLICANT: Bennett, C. Frank
 ; APPLICANT: Freier, Susan M.
 ; APPLICANT: Griffey, Richard H.
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: Vickers, Timothy
 ; APPLICANT: Marcussen, Eric G.
 ; APPLICANT: Koller, Erich
 ; APPLICANT: Swayze, Eric
 ; APPLICANT: Jain, Ravi
 ; APPLICANT: Bhat, Balkrishen
 ; APPLICANT: Peralta, Eigen
 ; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
 ; TITLE OF INVENTION: Of Small Non-Coding RNAs
 ; FILE REFERENCE: IS10080-100 (CORE016US)
 ; CURRENT APPLICATION NUMBER: US/10/909,125
 ; CURRENT FILING DATE: 2004-07-30
 ; PRIOR APPLICATION NUMBER: US 60/492,056
 ; PRIOR FILING DATE: 2003-07-31
 ; PRIOR APPLICATION NUMBER: US 60/516,303
 ; PRIOR FILING DATE: 2003-10-31
 ; PRIOR APPLICATION NUMBER: US 60/531,596
 ; PRIOR FILING DATE: 2003-12-19
 ; PRIOR APPLICATION NUMBER: US 60/562,417
 ; CURRENT FILING DATE: 2004-04-14
 ; NUMBER OF SEQ ID NOS: 2184
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 269
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: H. sapiens
 ; US-10-909-125-369

Query Match 100.0%; Score 22; DB 10; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; APPLICANT: Esau, Christine
 QY 1 UAGCAGCACAUAAUGGUUUG 22
 Db 1 UAGCAGCACAUAAUGGUUUG 22

RESULT 8
 US-10-881-362B-7
 ; Sequence 7, Application US/10881362B
 ; Publication No. US20060003337A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Applied Biosystems
 ; TITLE OF INVENTION: Detection of Small RNAs
 ; FILE REFERENCE: 962-00046
 ; CURRENT APPLICATION NUMBER: US/10/881,362B
 ; CURRENT FILING DATE: 2004-06-30
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 7
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Human
 ; US-10-881-362B-7

Query Match 100.0%; Score 22; DB 11; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; APPLICANT: Esau, Christine
 QY 1 UAGCAGCACAUAAUGGUUUG 22
 Db 1 UAGCAGCACAUAAUGGUUUG 22

RESULT 9
 US-11-055-035-16
 ; Sequence 16, Application US/11055035
 ; Publication No. US20050256072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aronin, Neil
 ; APPLICANT: Zamore, Phillip D.
 ; APPLICANT: Broderick, Jennifer
 ; TITLE OF INVENTION: DUAL FUNCTIONAL OLIGONUCLEOTIDES FOR USE IN REPRESSING
 ; TITLE OF INVENTION: MUTANT GENE EXPRESSION
 ; FILE REFERENCE: UMY-095
 ; CURRENT APPLICATION NUMBER: US/11/055,035
 ; CURRENT FILING DATE: 2005-02-09
 ; PRIOR APPLICATION NUMBER: 60/543,467
 ; PRIOR FILING DATE: 2004-02-09

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; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 16
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
;US-11-035-035-16

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 10
US-11-102-453-15
; Sequence 15, Application US/11102453
; Publication No. US20050260648A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; APPLICANT: Zammattéo, Nathalie
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR FILE REFERENCE: KLAUS2.06CP1
; CURRENT APPLICATION NUMBER: US/11/102,453
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/818,956
; PRIOR FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
;US-11-102-453-15

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 11
US-11-102-453-111
; Sequence 11, Application US/11102453
; Publication No. US20050260648A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; APPLICANT: Zammattéo, Nathalie
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR FILE REFERENCE: KLAUS2.06CP1
; CURRENT APPLICATION NUMBER: US/11/102,453
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/818,956
; PRIOR FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Mus musculus
;US-11-102-453-111

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 12
US-11-100-897-5
; Sequence 5, Application US/11100897
; Publication No. US20050272075A1
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, Nana
; APPLICANT: Kongsbak, Lars
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Etchwald, Soren Morgensthaler
; APPLICANT: Mouritzen, Peter
; APPLICANT: Nielsen, Peter Steen
; APPLICANT: Norholm, Mikkel
; TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF microRNAs AND SMALL FILE REFERENCE: 50287/013004
; CURRENT APPLICATION NUMBER: US/11/100,897
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/648,221
; PRIOR APPLICATION NUMBER: 60/619,291
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/600,961
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/590,856
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/560,148
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE: OTHER INFORMATION: Synthetic sequence
;US-11-100-897-5

Query Match 100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 68.2%; Pred. No. 1.9; Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 13
US-11-100-897-7
; Sequence 7, Application US/11100897
; Publication No. US20050272075A1
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, Nana
; APPLICANT: Kongsbak, Lars
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Etchwald, Soren Morgensthaler
; APPLICANT: Mouritzen, Peter
; APPLICANT: Nielsen, Peter Steen
; APPLICANT: Norholm, Mikkel
; TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF microRNAs AND SMALL FILE REFERENCE: 50287/013004
; CURRENT APPLICATION NUMBER: US/11/100,897
; CURRENT FILING DATE: 2005-04-07

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RESULT 15
 ;
 ; PRIOR APPLICATION NUMBER: 60/548, 221
 ; PRIOR FILING DATE: 2005-01-28
 ; PRIOR APPLICATION NUMBER: 60/619, 291
 ; PRIOR FILING DATE: 2004-10-15
 ; PRIOR APPLICATION NUMBER: 60/600, 961
 ; PRIOR FILING DATE: 2004-08-12
 ;
 ; PRIOR APPLICATION NUMBER: 60/590, 856
 ; PRIOR FILING DATE: 2004-07-23
 ; PRIOR APPLICATION NUMBER: 60/560, 148
 ; PRIOR FILING DATE: 2004-04-07
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 7
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: artificial sequence
 ; FEATURE: OTHER INFORMATION: Synthetic sequence
 ; US-11-100-897-7
 ;
 Query Match 100.0%; Score 22; DB 15; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 UAGCAGCACAUAAUGGUUGUG 22
 Db 1 UAGCAGCACAUAAUGGUUGUG 22

RESULT 14
 ;
 ; Sequence 73, Application US/11100897
 ; Publication No. US20050272075A1
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Jacobsen, Nana
 ; APPLICANT: Kongsbak, Lars
 ; APPLICANT: Kauppinen, Sakari
 ; APPLICANT: Eichwald, Soren Morgensthaler
 ; APPLICANT: Mouritzen, Peter
 ; APPLICANT: Nielsen, Peter Stein
 ; APPLICANT: Norholm, Mikkel
 ;
 ; TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF miRNAs AND SMALL
 ; TITLE OF INVENTION: INTERFERING RNAs
 ; FILE REFERENCE: 50287/013004
 ; CURRENT APPLICATION NUMBER: US/11/100, 897
 ;
 ; CURRENT FILING DATE: 2005-04-07
 ;
 ; PRIOR APPLICATION NUMBER: 60/648, 221
 ;
 ; PRIOR FILING DATE: 2005-01-28
 ;
 ; PRIOR APPLICATION NUMBER: 60/619, 291
 ;
 ; PRIOR FILING DATE: 2004-10-15
 ;
 ; PRIOR APPLICATION NUMBER: 60/600, 961
 ;
 ; PRIOR FILING DATE: 2004-08-12
 ;
 ; PRIOR APPLICATION NUMBER: 60/550, 856
 ;
 ; PRIOR FILING DATE: 2004-07-23
 ;
 ; PRIOR APPLICATION NUMBER: 60/560, 148
 ;
 ; PRIOR FILING DATE: 2004-04-07
 ;
 ; NUMBER OF SEQ ID NOS: 79
 ;
 ; SOFTWARE: PatentIn version 3.3
 ;
 ; SEQ ID NO: 73
 ; LENGTH: 22
 ;
 ; TYPE: RNA
 ;
 ; ORGANISM: Homo sapiens
 ;
 ; US-11-100-897-73
 ;
 Query Match 100.0%; Score 22; DB 15; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: November 2, 2006, 02:46:33
 Job time : 528.371 secs

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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 22:25:14 ; Search time 49.6571 seconds

(without alignments)

859.641 Million cell updates/sec

Title: US-10-706-798-3
Perfect score: 22
Sequence: 1 uagcagcacauaauugguugug 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2461376 seqs, 970166171 residues

Total number of hits satisfying chosen parameters: 4922752

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:/*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:/*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:/*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PTCT_NEW_PUB.seq:/*
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10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query

Match Length DB ID

Description

RESULT 1

US-10-818-956-15

; Sequence 15, Application US/10818956

; Publication No. US20060134639A1

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match 100.0%; Score 22; DB 6; Length 22;

; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;

; Matches 22; Conservative 0; ;

; GENERAL INFORMATION:

; APPLICANT: Van Huffel, Christophe

; ATTORNEY: Remacle, Jose

; ATTORNEY: Bulow, Sven

; ATTORNEY: Zammattie, Nathalie

; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION

; FILE REFERENCE: KLAUS2_006AUS

; CURRENT APPLICATION NUMBER: US/10/818,956

; CURRENT FILING DATE: 2004-04-06

; NUMBER OF SEQ ID NOS: 212

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 15

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Homo Sapiens

; US-10-818-956-15

; Query Match

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Mus musculus
; US-10-818-956-111
; Query Match 100.0%; Score 22; DB 6; Length 22;
; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 UAGCACGCCACAUAAUGGUUUGUG 22
; Db 1 UAGCACGCCACAUAAUGGUUUGUG 22

RESULT 3
; US-11-317-660-36
; Sequence 36, Application US/11317660
; Publication No. US20060185027A1
; GENERAL INFORMATION:
; APPLICANT: BARTEL, DAVID P.
; APPLICANT: JONES-RHODES, MATTHEW W.
; APPLICANT: LEWIS, BENJAMIN P.
; APPLICANT: BURKE, CHRISTOPHER B.
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR IDENTIFYING miRNA TARGETS
; TITLE OF INVENTION: AND FOR ALTERING miRNA AND TARGET EXPRESSION
; FILE REFERENCE: WO571.70013US01
; CURRENT APPLICATION NUMBER: US/11/317,660
; CURRENT FILING DATE: 2005-12-23
; PRIORITY APPLICATION NUMBER: 60/639,231
; PRIOR FILING DATE: 2004-12-23
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; US-11-317-660-36
; Query Match 100.0%; Score 22; DB 7; Length 22;
; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 UAGCACGCCACAUAAUGGUUUGUG 22
; Db 1 UAGCACGCCACAUAAUGGUUUGUG 22

RESULT 4
; US-11-317-660-795/C
; Sequence 795, Application US/11317660
; Publication No. US20060185027A1
; GENERAL INFORMATION:
; APPLICANT: BARTEL, DAVID P.
; APPLICANT: JONES-RHODES, MATTHEW W.
; APPLICANT: LEWIS, BENJAMIN P.
; APPLICANT: BURKE, CHRISTOPHER B.
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR IDENTIFYING miRNA TARGETS
; TITLE OF INVENTION: AND FOR ALTERING miRNA AND TARGET EXPRESSION
; FILE REFERENCE: WO571.70013US01
; CURRENT APPLICATION NUMBER: US/11/317,660
; CURRENT FILING DATE: 2005-12-23
; PRIORITY APPLICATION NUMBER: 60/639,231
; PRIOR FILING DATE: 2004-12-23
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 795
; LENGTH: 22
; TYPE: RNA

RESULT 5
; US-11-084-082-2
; Sequence 2, Application US/11084082
; Publication No. US20060211000A1
; GENERAL INFORMATION:
; APPLICANT: SORGE, JOSEPH A.
; APPLICANT: MULLINAX, REBECCA L.
; TITLE OF INVENTION: METHODS, COMPOSITIONS, AND KITS FOR DETECTION OF
; FILE REFERENCE: STG-114
; CURRENT APPLICATION NUMBER: US/11/084,082
; CURRENT FILING DATE: 2005-03-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: PatentIn Ver. 3.3
; US-11-084-082-2
; Query Match 100.0%; Score 22; DB 7; Length 22;
; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 UAGCACGCCACAUAAUGGUUUGUG 22
; Db 1 UAGCACGCCACAUAAUGGUUUGUG 22

RESULT 6
; US-11-084-082-27
; Sequence 27, Application US/11084082
; Publication No. US20060211000A1
; GENERAL INFORMATION:
; APPLICANT: SORGE, JOSEPH A.
; APPLICANT: MULLINAX, REBECCA L.
; TITLE OF INVENTION: METHODS, COMPOSITIONS, AND KITS FOR DETECTION OF
; FILE REFERENCE: STG-114
; CURRENT APPLICATION NUMBER: US/11/084,082
; CURRENT FILING DATE: 2005-03-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 27
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: PatentIn Ver. 3.3
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; US-11-084-082-27
; Query Match 100.0%; Score 22; DB 7; Length 22;
; Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAAUGGUUUGUG 22
 US-11-242-139-31
 ; Sequence 31, Application US/11242139
 ; Publication No. US20060099619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: REMACLE, JOSE
 ; APPLICANT: DU LONGEVILLE, FRANCOISE
 ; APPLICANT: HAMEL, SANDRINE
 ; TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF miRNA ON MICRO-ARRAYS
 ; FILE REFERENCE: 035442-0107
 ; CURRENT APPLICATION NUMBER: US/11242,139
 ; CURRENT FILING DATE: 2005-10-04
 ; PRIORITY APPLICATION NUMBER: 10/637,656
 ; PRIORITY FILING DATE: 2003-08-11
 ; NUMBER OF SEQ ID NOS: 239
 ; SEQ ID NO: 31
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-11-242-139-31

Query Match 100.0%; Score 22; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAAUGGUUUGUG 22
 Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 8
 US-11-242-139-127
 ; Sequence 127, Application US/11242139
 ; Publication No. US20060099619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: REMACLE, JOSE
 ; APPLICANT: DU LONGEVILLE, FRANCOISE
 ; APPLICANT: HAMEL, SANDRINE
 ; TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF miRNA ON MICRO-ARRAYS
 ; FILE REFERENCE: 035442-0107
 ; CURRENT APPLICATION NUMBER: US/11/242,139
 ; CURRENT FILING DATE: 2005-10-04
 ; PRIORITY APPLICATION NUMBER: 10/637,656
 ; PRIORITY FILING DATE: 2003-08-11
 ; NUMBER OF SEQ ID NOS: 239
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 127
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Mus musculus
 ; US-11-242-139-127

Query Match 100.0%; Score 22; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAAUGGUUUGUG 22
 Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 9
 US-11-375-650-3
 ; Sequence 31, Application US/11242139
 ; Publication No. US20060099619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Croce, Carlo M.
 ; APPLICANT: Calin, George A.
 ; TITLE OF INVENTION: Compositions and Methods for Cancer
 ; FILE REFERENCE: 0321-0126US1
 ; CURRENT APPLICATION NUMBER: US/11/375,650
 ; CURRENT FILING DATE: 2006-03-13
 ; PRIORITY APPLICATION NUMBER: US/10/706,798
 ; PRIORITY FILING DATE: 2003-11-12
 ; PRIORITY APPLICATION NUMBER: 60/4425,864
 ; PRIORITY FILING DATE: 2002-11-13
 ; PRIORITY APPLICATION NUMBER: 60/469,464
 ; PRIORITY FILING DATE: 2003-05-09
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-11-375-650-3

Query Match 100.0%; Score 22; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.093; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAAUGGUUUGUG 22
 Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 10
 US-11-194-055-325
 ; Sequence 325, Application US/11194055
 ; Publication No. US20060105360A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Croce, Carlo M.
 ; APPLICANT: Liu, Chang-Gong
 ; APPLICANT: Calin, George A.
 ; APPLICANT: Cinzia, Sevignani
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
 ; TITLE OF INVENTION: miRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
 ; TITLE OF INVENTION: FEATURES
 ; CURRENT APPLICATION NUMBER: US/11/194,055
 ; CURRENT FILING DATE: 2005-07-29
 ; PRIORITY APPLICATION NUMBER: PCT/US2005/004865
 ; FILE REFERENCE: 3599.1018-008
 ; PRIORITY APPLICATION NUMBER: 60/543,119
 ; PRIORITY FILING DATE: 2005-02-09
 ; PRIORITY APPLICATION NUMBER: 60/543,119
 ; PRIORITY FILING DATE: 2004-02-09
 ; PRIORITY APPLICATION NUMBER: 60/542,929
 ; PRIORITY FILING DATE: 2004-02-09
 ; PRIORITY APPLICATION NUMBER: 60/542,963
 ; PRIORITY FILING DATE: 2004-02-09
 ; PRIORITY APPLICATION NUMBER: 60/542,940
 ; PRIORITY FILING DATE: 2004-02-09
 ; PRIORITY APPLICATION NUMBER: 60/5580,959
 ; PRIORITY FILING DATE: 2004-06-18
 ; PRIORITY APPLICATION NUMBER: 60/5580,797
 ; PRIORITY FILING DATE: 2004-06-18
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 325
 ; LENGTH: 40
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide probe
 ; US-11-194-055-325

Query Match 100.0%; Score 22; DB 8; Length 40;
 Best Local Similarity 68.02%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAAUGGUUUGUG 22
 Db 1 UAGCAGCACAUAAUGGUUUGUG 22

; PRIOR FILING DATE: 2004-06-18
 ; NUMBER OF SEQ ID NOS: 6/3
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO: 32
 ; LENGTH: 108
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-11-194-055-32

Query Match 100.0%; Score 22; DB 8; Length 108;
 Best Local Similarity 68.2%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UAGCAGCACAUAAUUGGUUUGUG 22
 Db 43 TAGGAGCATAATGTTGTCG 64

RESULT 15
 US-11-266-748A-23474/C
 ; Sequence 23474, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; TITLE OF INVENTION: Methods of Using the Same
 ; CURRENT APPLICATION NUMBER: US11-266,748A
 ; CURRENT FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 2344
 ; LENGTH: 347503
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; US-11-266-748A-23474

Query Match 100.0%; Score 22; DB 8; Length 347503;
 Best Local Similarity 68.2%; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGCAGCACAUAAUUGGUUUGUG 22
 Db 52185 TAGGAGCATAATGTTGTCG 52164

Search completed: November 1, 2006, 22:36:58
 Job time : 50.6571 secs

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